

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:04:22 ; Search time 52 Seconds
(without alignments)
4908.735 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSTTKNVKVPICGNNEN.....PSAEGGEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	4234	100.0	809 4 Q9NQW8	Q9NQW8 homo sapien
2	3181.5	75.1	782 6 Q8MJD7	Q8mjd7 canis famil
3	3166.5	74.8	610 4 Q9NRE9	Q9NRE9 homo sapien
4	2515	59.4	694 11 Q9JUZ9	Q9jiz9 mus musculus
5	1971.5	46.6	866 11 Q80XL8	Q80xl8 mus musculus
6	1959	46.3	1339 11 Q35788	Q35788 rattus norv
7	1952	46.1	1245 4 Q43636	Q43636 homo sapien
8	1949	46.0	1251 4 Q9UMG2	Q9umg2 homo sapien
9	1923	45.4	858 11 Q55157	Q55157 rattus norv
10	1920	45.3	938 6 Q77659	Q77659 bos taurus
11	1920	45.3	948 6 Q77659	Q77659 bos taurus
12	1920	45.3	952 6 Q77650	Q77650 bos taurus
13	1103	26.1	1037 5 Q9W2D5	Q9w2d5 drosophila
14	1103	26.1	1040 5 Q8IH43	Q8ih43 drosophila
15	1096	25.9	800 5 P90975	P90975 caenorhabdi
16	1095	25.9	800 5 Q62237	Q62237 caenorhabdi

17	878	20.7	515	5	Q95SL0
18	818	19.3	686	6	Q9N0H4
19	806	19.0	611	11	Q9QWN7
20	806	19.0	632	11	Q9ER32
21	806	19.0	670	11	Q9ER33
22	789.5	18.6	664	11	Q80XH6
23	788.5	18.6	631	11	Q8CFV6
24	787.5	18.6	1218	5	Q9W201
25	783.5	18.5	637	13	Q804I6
26	759	17.9	1463	5	Q9USE2
27	746	17.6	900	5	Q971I9
28	723	17.1	1324	5	Q8IR35
29	714.5	16.9	737	13	Q8UVT8
30	712	16.8	609	13	Q8JFP0
31	703	16.6	551	13	Q8JFN9
32	702.5	16.6	310	11	Q80VQ4
33	702	16.6	1696	5	Q9VXV8
34	621	14.7	147	11	Q9QWK1
35	563.5	13.3	695	5	Q93486
36	536	12.7	474	4	Q8IV77
37	509	12.0	832	5	Q9N4C1
38	478	11.3	252	11	Q9QX26
39	441.5	10.4	644	5	Q61827
40	400	9.4	774	4	Q86WJ5
41	383	9.0	945	5	Q971J9
42	383	9.0	1327	5	Q9V702
43	381	9.0	678	5	Q96777
44	375	8.9	767	5	Q76977
45	369.5	8.7	890	4	Q86WJ6

ALIGNMENTS

RESULT 1

ID	Q9NQW8	PRELIMINARY;	PRT;	809 AA.
AC	Q9NQW8;			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)			
DE	Cone photoreceptor cyclic nucleotide-gated channel beta subunit.			
GN	CNGB3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20414632; PubMed=10958649;			
RA	Kohl S., Baumann B., Broghammer M., Jagle H., Sieving P., Kellner U.,			
RA	Spegal R., Anastasi M., Zrenner E., Sharpe L.T., Missinger B.,			
RT	"Mutations in the CNGB3 gene encoding the Beta-subunit of the cone			
RT	photoreceptor cGMP-gated channel are responsible for achromatopsia			
RT	(ACHM3) linked to chromosome 8Q21."			
RL	Hum. Mol. Genet. 9:2107-2116(2000).			
DR	EMBL; AF272900; AAF66274.1; --			
DR	Genew; HGNC:2153; CNGB3.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005216; F:ion channel activity; IEA.			
DR	GO; GO:0005267; F:potassium channel activity; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0006811; P:ion transport; IEA.			
DR	GO; GO:0006813; P:potassium ion transport; IEA.			
DR	InterPro; IPR000595; CNMP_binding.			
DR	InterPro; IPR005821; Ion_trans.			
DR	InterPro; IPR001622; K+channel_pore.			
DR	Pfam; PF00027; CNMP_binding; 1.			
DR	Pfam; PF00320; ion_trans; 1.			
DR	SMART; SM00100; CNMP; 1.			
DR	PROSITE; PS00888; CNMP_BINDING_1; 1.			
DR	PROSITE; PS00889; CNMP_BINDING_2; 1.			
DR	PROSITE; PS00842; CNMP_BINDING_3; 1.			

QY 599 GGNRRRTANVAHGFANLTLTKTQELVHYVPSERILMKARVLLKQKAKTAEATPP 658
 Db 594 RGNRRRTANVAHGFANLTLTKTQELVHYVPSERILMKARVLLKQKAKTAEATPP 653
 QY 659 RGDALLFPKKEPTKLFKTLGGTGKASIALRLKLKREQAOKKENSSEGGEEKENED 718
 Db 654 RKGALFPPKQETPKFKAJGGTGKAGLTLKLKREQTQK--TSNSEGG----- 706
 QY 719 KOKENEDKOKENEDKOKENEDKOGREPEKPLDRPECTASPIAVEEPPHVRRTVLPKG 778
 Db 707 -----GKREYEDKEREPESEKILDSSECRANCIIEEMPOQSIRRAALPRG 751
 QY 779 TSQSLSIISNAPSABGSEVLTIEVKEKAKQ 809
 Db 752 TTSQSLSIISNAPSABGSEVLTIEVKEKAKQ 782

RESULT 3

ID Q9NR9 PRELIMINARY; PRT; 610 AA.
 AC Q9NR9;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Cone photoreceptor cGMP-gated cation channel beta-subunit.
 GN CNGB3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=20347712; PubMed=10888875;
 RA Sundin O.H., Yang J.-M., Li Y., Zhu D., Hurd J.N., Mitchell T.H.,
 RA Silva E.D., Maumenee I.H.;
 RT "Genetic basis of total colourblindness among the Pingelapese
 islanders.";
 RL Nat. Genet. 25:289-293(2000).
 DR ENBL; AF228520; AAF80179.1;
 DR GO; GO:0007601; P:vision; TAS.
 DR InterPro; IPR000591; cGMP binding.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR Pfam; PF00027; cGMP binding; 1.
 DR Pfam; PF00520; ion trans; 1.
 DR SMART; SM00100; cGMP; 1.
 DR PROSITE; PS00889; CNMP_BINDING_1; 1.
 DR PROSITE; PS50042; CNMP_BINDING_3; 1.
 KW Ionic channel; Receptor; Transmembrane.
 SQ SEQUENCE 610 AA; 70039 MW; 843801F12643B73A CRC64;

Query Match 74.8%; Score 3166.5; DB 4; Length 610;
 Best Local Similarity 99.0%; Pred. No. 5.7e-214;
 Matches 609; Conservative 0; Mismatches 1; Indels 5; Gaps 1;
 QY 195 MPEYLKRIKLPNSIDSYDRLYLMLLVTLAYNWNCFIPLRLVFPYQTADNIHYWL 254
 Db 1 MPEYLKRIKLPNSIDSYDRLYLMLLVTLAYNWNCFIPLRLVFPYQTADNIHYWL 60
 QY 255 IADIICDIYLYDMLFQPLQFVRGDDIIVDSNELKHYRTSTKQLDVASIIIPEDICY 314
 Db 61 IADIICDIYLYDMLFQPLQFVRGDDIIVDSNELKHYRTSTKQLDVASIIIPEDICY 120
 QY 315 LFFGFNPMFRANRMLKYSFPFNFHLESIMDKAYIVRVRTTGYLLFILHINACYVYWA 374
 Db 121 LFFGFNPMFRANRMLKYSFPFNFHLESIMDKAYIVRVRTTGYLLFILHINACYVYWA 180
 QY 375 SNVEGIGTRWYDGEENYLCRYWAVRLLITIGLPEPQTLFEIVFQLLNFPFGVVF 434
 Db 181 SNVEGIGTRWYDGEENYLCRYWAVRLLITIGLPEPQTLFEIVFQLLNFPFGVVF 240

QY 435 SSLIGQMRDVGATANONYFRACMDDTIAYMNNYSIPKLVOKEVRTWYETWDSQRMLD 494
 Db 241 SSLIGQMRDVGATANONYFRACMDDTIAYMNNYSIPKLVOKEVRTWYETWDSQRMLD 300
 QY 495 ESDLLKTLPTTVQALALADYNFISIISKVDLFGKCDTQMIYDMLRLKSLVLYLPGDFVCKK 554
 Db 301 ESDLLKTLPTTVQALALADYNFISIISKVDLFGKCDTQMIYDMLRLKSLVLYLPGDFVCKK 360
 QY 555 GEIKEMWIIKHGBVQVVGPDGTGYLVTLKAGSVFGEISLLAAGGNGRRRTANVAHGA 614
 Db 361 GEIKEMWIIKHGBVQVVGPDGTGYLVTLKAGSV-----LLAAGGNGRRRTANVAHGA 415
 QY 615 NLLTLDKKTQELIIVHYVPSERILMKARVLLKQKAKTAEATPPKDLALLFPKKEETPK 674
 Db 416 NLLTLDKKTQELIIVHYVPSERILMKARVLLKQKAKTAEATPPKDLALLFPKKEETPK 475
 QY 675 LFKTLGGTGKASIALRLKLKREQAOKKENSSEGGEEKENEDKOKENEDKOG 734
 Db 476 LFKTLGGTGKASIALRLKLKREQAOKKENSSEGGEEKENEDKOKENEDKOG 535
 QY 735 KENEDKOGREPEKPLDRPECTASPIAVEEPPHVRRTVLPRTSRSQSLSIISNAPSABG 794
 Db 536 KENEDKOGREPEKPLDRPECTASPIAVEEPPHVRRTVLPRTSRSQSLSIISNAPSABG 595
 QY 795 GEEVLTIEVKEKAKQ 809
 Db 596 GEEVLTIEVKEKAKQ 610

RESULT 4

ID Q9JZ9 PRELIMINARY; PRT; 694 AA.
 AC Q9JZ9;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Cyclic nucleotide-gated channel subunit CNG6.
 GN CNGB3 OR CNG6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=c57BL/6J;
 RX MEDLINE=20130348; PubMed=10662822;
 RA Gerstner A., Zong X., Hofmann F., Biel M.;
 RT "Molecular Cloning and Functional Characterization of a New Modulatory
 RT Cyclic Nucleotide-Gated Channel Subunit from Mouse Retina.";
 RL J. Neurosci. 20:1324-1332(2000).
 DR EMBL; AF243572; CAB71152.1; -.
 DR MGD; MGI:1353562; Cngb3.
 DR GO; GO:0005886; C:plasma membrane; IC.
 DR GO; GO:0030553; F:3',5'-cGMP binding; IC.
 DR GO; GO:0005223; F:intracellular cGMP activated cation channel. .; IPI.
 DR GO; GO:0003187; P:cyclic nucleotide metabolism; IC.
 DR InterPro; IPR000595; cGMP_binding.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR Pfam; PF00027; cGMP binding; 1.
 DR Pfam; PF00520; ion trans; 1.
 DR SMART; SM00100; cGMP; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; 1.
 DR PROSITE; PS00889; CNMP_BINDING_2; 1.
 DR PROSITE; PS00842; CNMP_BINDING_3; 1.
 KW Ionic channel; Transmembrane.
 SQ SEQUENCE 694 AA; 79722 MW; 0B9F9CF3B180DA82 CRC64;

Query Match 59.4%; Score 2515; DB 11; Length 694;
 Best Local Similarity 68.7%; Pred. No. 4.1e-168;
 Matches 485; Conservative 92; Mismatches 113; Indels 16; Gaps 7;
 QY 1 MFPSLIT-KVNYKPIGNNENESQSRREBEGSH--SNQSQQTAAEENKGEKSLTKYS 57

Db 1 MLKSLTVKFNKVPNPM-----EGRMKKLCPNLSSLSQPTIAQGNQSEKPELRSR- 50
Qy 58 TPVTSEEPHTNIQDKLSKNSGDLTTPDPQNAABPTGIVPEQKMDPGKEGNSPQNK 117
Db 51 TPITFEKSHSK-EDNSTGNSLDFTPNPDPECAELTRTMAEKEKTRTKGERPVSKTK 109
Qy 118 PPAAPVINEYADAQHNLVKKMRORTALYKXKLVGEGD-LSSPEASPOKAPTAVPPVKES 176
Db 110 VLETSIINEYTDALHNLVRRERTALYKXKLTLEENFPEVEASSQTAMSTWISPKQEN 169
Qy 177 DDKPTEHYRLLWFKVKVKKMPTEYLKRIKLNSIDSTDRLLYLWLLLVLTAYNNWCWF 236
Db 170 NSKLEH-QDTFSFKPQRPVKEHLRRMLPRSDISYTDVYLLWLLLVLTAYNNWCWLL 228
Qy 237 PLRLVFPYQTDADNTHYWLIADIIIDYVLMFIQRLQVPGDGIIVDSNELRKHRT 296
Db 229 PVLVFPQCTDNKYWIITDVIDIYLDLILQRLQVPGGEIIVDSNELKRYRS 288
Qy 297 STKQOLDVASIIPEDICYLFGFNPFRANRLKXKTSFFPNHLESIMDKAVYRVIRT 356
Db 289 STKFRMDVASLLPEVLYIFGVPNPIFRANRLKXKTSFFPNHLESIMDKAVYRVIRT 348
Qy 357 TGYLLFLHINACVYVNASVEGIGTRWYVDGNEYLRYWAVTLITIGLPEPOT 416
Db 349 TGYLLFLHINACVYVNASVEGIGTRWYVDGNEYLRYWAVTLITIGLPEPOT 408
Qy 417 LFEIVFQNLNFGSVFSSLIQMDVIGAAATANQNYFRACMDDTIAYNNYSIPKLQV 476
Db 409 SFEIVFQNLNFGSVFSSLIQMDVIGAAATANQNYFRACMDHIAYNNYSIPQSVQ 468
Qy 477 KRVTWYTWDSORMDESLKTLTPTVOLALADVNSIISKVDLFGKCDTQMIDM 536
Db 469 YRVTWLEWYNSORILDESLENLEPTAQSLDALDINFSIIDKVELFPGKCDTQMIDL 528
Qy 537 LLRLKSLVILPGDFCKGKEIGKEMWIIKGEVOVLGGPDGTGKVLTKAGSVFGEISLL 596
Db 529 LLRLKSLVILPGDFCKGKEIGKEMWIIKGEVOVLGGPDGTGKVLTKAGSVFGEISLL 588
Qy 597 AAGGNRTANVAHGFAANILTDKTLQBIIVHPDSERILMKKARVLKQAKATAEAT 656
Db 589 AKGGNRTADVVAHGFAANILTDKTLQBIIVHPDSERILMKKARVLKQAKATAEAT 648
Qy 657 PPRKDLALLPPKKEETPKLTKTLGGTKASLAFLLKXEQAAQK 702
Db 649 PARPGPALFPKKEETPKLTKTLGGTKASLAFLLKXEQAAQK 694

RESULT 5

Q80XL8 PRELIMINARY; PRT; 866 AA.
AC Q80XL8
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE LOC333329 protein (Fragment).
GN LOC333329.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Eve;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heltan E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eve;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045114; AHA45114.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; P:ion channel activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000595; C:GMP binding.
DR InterPro; IPR005821; I:ion trans.
DR InterPro; IPR000531; TonB boxC.
DR Pfam; PF00027; C:GMP binding; 1.
DR Pfam; PF00520; I:ion trans; 1.
DR SMART; SM00100; C:GMP; 1.
DR PROSITE; PS00888; C:GMP BINDING_1; 1.
DR PROSITE; PS00889; C:GMP BINDING_2; 1.
DR PROSITE; PS00442; C:GMP BINDING_3; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
DR NON TER 1
SQ SEQUENCE 866 AA; 97427 MW; CACC4AD8EBDEE2A CRC64;
Query Match 46.6%; Score 1971.5; DB 11; Length 866;
Best Local Similarity 47.5%; Pred. No. 8.5e-130;
Matches 406; Conservative 107; Mismatches 247; Indels 95; Gaps 14;
Qy 21 EOSSRRNEEGSHPSNQSQTAAQENKGEESLTKTPTVTSEEPHTNIQDKLSKNSG 80
Db 38 EKE 94
Qy 81 DL-----TTNPDQNAABPTGIVPEQKMDPGKEGPN-----SPQNKPPAA 121
Db 95 FLIPEETLPPPERPPSPVKSDTLTPGAAAAGHRKKLPQSDDEAEELKALSPAESPVA 154
Qy 122 ---PVINEYADAQ-----LHNLVKKMRQRTALYKXKLVGEGDLSPEAS 161
Db 155 WSDPTTPOEADGQDRAASTASQNSALINDRLQELVKMFKEKTEKVKELIDPDVTSDES 214
Qy 162 PQAKPTAVPPVKESDDKPT-----EHYRLLVKKMKMPLTEYLKRIKLNSIDSYT 214
Db 215 PKPS-PAKKAPEPDPAPKAEVAEEHEDYCDLCKFKRRLPNY---RFQSIDPLT 269
Qy 215 DRVLLWLLLVLTAYNNWCWIPRLVPPYOTADNIHVLIIADIIIDYVLMFIQRL 274
Db 270 NLMLWLLFFVVLANNWCWIPVWAFPYORADNIHVLIIADIIIDYVLMFIQRL 329
Qy 275 LQFVRGGDIIIVDSNELRKHRTSTKFDQVVASIIPFDICYLFGFNPFRANRLKXKTSF 334
Db 330 LQFVRGGDIIIVDSNELRKHRTSTKFDQVVASIIPFDICYLFGFNPFRANRLKXKTSF 389
Qy 335 FEENHLESIMDKAVYRVIRTTCYLLFILHINACVYVNASVEGIGTRWYVDGNEGY 394
Db 330 FEENHLESIMDKAVYRVIRTTCYLLFILHINACVYVNASVEGIGTRWYVDGNEGY 449
Qy 395 LRCYVAVRTLITIGLPEPOTLEFVQLNFGFSSLIQMDVIGAAATANQNYFRACMD 454
Db 450 LRCYVAVRTLITIGLPEPOTLEFVQLNFGFSSLIQMDVIGAAATANQNYFRACMD 509
Qy 455 FRACMDDTIAYNNYSIPKLTKGKRTWYETWDSQRMDESLKTLTPTVOLALADV 514

DR PROSITE; P550042; CNMP_BINDING_3; 1.
SQ Ionic channel; Transmembrane.
KW SEQUENCE 948 AA; 105212 MW; 1DA77400115C2074 CRC64;

Query Match 45.3%; Score 1920; DB 6; Length 948;
Best Local Similarity 45.9%; Pred. No. 4e-126;
Matches 401; Conservative 118; Mismatches 242; Indels 112; Gaps 17;

QY 15 GENNEEQSRNREGSHPSNQOQTAAEENKGEKSILKTSTPTVEEPHTNIQDK-- 72
DB :
QY 86 GAQAQGEVGAQGDGVGGA-QDQSTSHQELQ--BEALADSSGVPAPEEHPELQVEDADA 142
DB :
QY 73 -----LSKNSSGDLTTNPDPQNAEAAPTCTVP-----EQEMDPGK 108
DB :
DB 143 DSRPLTAENPPSPVOLPLSP--AKSDTLAVPGSATGSLRKRLPSQDDAEELKMLSPAA 200
QY 109 -----EGNSPQNKPFA-----APVINEYADAQLHNLVKRMQORTALYKKKLVE 152
DB :
DB 201 SPVAVMSDTPSGTDDQDTRATSTASQNSAIIND----RLQELVKLFKERTKEVKEKLID 256
QY 153 GDLS-----SPEASPQTAKTAVPVVK--ESDDKPTHEYRYLLFWFKWMLTEYLKRKL 206
DB :
DB 257 PDVTSEESPSPKAPKAPEPAPEVKAPEGVEBEEHYCEMLCCCKFRPWPKKY----QF 312
QY :
QY 207 PNSIDSYTRLVLLMILLVLTAYNNWCWFIPIRLVFPYTADNIHYLIADIICDIIVLY 266
DB :
DB 313 PQSIDPLTNLMYLWLVFFVLAWNNCWLIPIVRWAFPYQTPDNIELMLMDVLCDLIYLL 372
QY 267 DMFLIQPRLOFVRGGDIIIVDSNELRKHRTSTKFOLDVASIIPPDICYLFGFNPMFRAN 326
DB :
DB 373 DITVFQMRLOFVRGGDIIIVDKEMRNYYKSORFYKMDMLCLLPDLLLYLKFGVNPLLRP 432
QY 327 RMLKYTSFFEHNHLESIMDKAYIVRVIRTTGYLLFILHINACVYMASNEGIGTTRWV 386
DB :
DB 433 RCLKYWAFPEFNNRLESILSKAYVVIETAYLLYSLHLNSCLYYMASAYEGLGSTHWV 492
QY 387 YDGEGNEYRCYVYAVRTLITIGGLEPOTLFEIVPOLLNPFSGVVFSSLIQNRDVIG 446
DB :
DB 493 YDVGNSYIRCYYVAWKLTITIGGLPDRTLFEIVFQGLNYFTGFVAFSVMIQMRDVYG 552
QY 447 AATAQNYPACMDDTIAVMNYSIPKLVQKRVRTWYETWDSQRMLDESLLKLTPTTV 506
DB :
DB 553 AATAGQTYRSOMDSIVKYNMFKIIPRSVQNRVKTWYEYTHWSQGMLDESELWQLPDKM 612
QY 507 QLALAIDVNFISIISVDLFGCDTQMIDYMLLRKLSVLYLPQDFYCKKGKEIKEMYIIKH 566
DB :
DB 613 RLDAIDVNSIVSKVALFOGCDROMIFDMKLRLSVVLYLPNDYVCCKGEIGREMYIIQA 672
QY 567 GEVOVLGGPCTKVLYTLTKAGSVFGEISLLAAGGNRRRTANVAVGFANLLTDKKTLOE 626
DB :
DB 673 GOVQVLGGPDGKSVLYTLTKAGSVFGEISLLAVGGNRRRTANVAVGFNTLFLDKKDLINE 732
QY 627 ILVHPDSEIRILMKARVLIKQAKTAETAPPKCOLALLFPKRETPKLFKTLGGTGKA 686
DB :
DB 733 ILVHPESQKLARKARRMLRNKK-----PKESVLTLPFRAGTFPKLFNAALAAAGKM 786
QY 687 SL-----ARLLKLREQAOKKENSEGGEKEKEDQKENEKQKEDNGK 734
DB :
DB 787 GAXGGRGRIALLRLARKELAALAAARQQOL---LEQAKSSEDAAVGSE-----G 834
QY 735 KENEDKQGREPREKPLDRPECTA-----SPIAVEEPHSVRTVLP 776
DB :
DB 835 SASPEQPPREPAPAPAPEPTAPLEAPAPAPAPSPPPASQERPEPGDKDAARP 894
QY 777 RGTSRQSLLISMAPSABGGSEVLTIEVKEKAKQ 809
DB :
DB 895 ---EEHVRIHVLGPDPSPQILLVEVPEKQEE 924

RESULT 12
O77660 PRELIMINARY; PRT; 952 AA.
ID O77660
AC O77660;

Db 617 RDLAIDVNVISVSKVALFQCSDQMFIMLKLRLSVVYLPNDYVCKGIGREMYIQA 676
Qy 567 GEVQVGLPGDQTKVLVILKAGSVGEISLLAAGGNNRTANVAHGPNLTLTKTQLQE 626
Db 677 GQVQVGLPGDQTKVLVILKAGSVGEISLLAAGGNNRTANVAHGPNLTLTKTQLQE 736
Qy 627 ILVHYPDSERILMKKARVLLKQAKTAEATPPRKDLALLPPKEETPKLTKTLGGTGA 686
Db 737 ILVHYPDSERILMKKARVLLKQAKTAEATPPRKDLALLPPKEETPKLTKTLGGTGA 790
Qy 687 SL-----ARLLKUREQAQKXENSEGEEGKEDKOKENEDKKG 734
Db 791 GAKGGRGRLALLRLKELAALAAARQOOL---LEQAKSSEDAVGE-----G 838
Qy 735 KENEDKKGPEEKPLDRECTA-----SPLAVEEPHVSRTVLP 776
Db 839 SASPEQPPPEPPAPEAPEPTAPEPLAPEAPEAPSSPPASQEPGDKDAARP 898
Qy 777 RGTSRQSLIISMAPSARGGSEVITIEYKKAQ 809
Db 899 --EEHPVRIHVTLGPPSPQILLVVEPKQEE 928
RESULT 13
Q9W2D5 PRELIMINARY; PRT; 1037 AA.
AC Q9W2D5
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE CG17922 protein.
GN CG17922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AE003454; AAF46752.1; --
DR FlyBase; FBgn0034656; CG17922.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; cAMP binding.
DR InterPro; IPR005821; IonTrans.
DR InterPro; IPR001622; K-channel pore.
DR Pfam; PF00027; cAMP binding; 1.
DR Pfam; PF00520; ion trans; 1.
DR SMART; SM00100; cAMP; 1.
DR PROSITE; PS00888; cAMP BINDING_1; 1.
DR PROSITE; PS00889; cAMP BINDING_2; 1.
DR PROSITE; PS00442; cAMP BINDING_3; 1.
KW Ionic channel; transmembrane.
SQ SEQUENCE 1037 AA; 118393 MW; FCFB7A1590E7F051 CRC64;
Query Match 26.1%; Score 1103; DB 5; Length 1037;
Best Local Similarity 33.4%; Pred. No. 1.1e-68;
Matches 243; Conservative 153; Mismatches 255; Indels 76; Gaps 13;
Qy 16 ENNEQSSRRNEGSHPSNOSQOTTAQ-----EENKGEKSLKTSPTVTSEETPNI 69
Db 276 EEEEEKSPLHVESQPDVDEQDVQICYNSEFELQNEEDRNETQRTPTSESEIVAV 335
Qy 70 QDKLSKNSGDLTTPDQNAEPTGTVPQEKMDPKGSPNSQNKPPAAPVINEYAD 129
Db 336 DEPTENMSVDV---HRKPSSA---GSLDSQGG-----OFLR 366
Qy 130 AQLHNLKRMQRORTALYKCKLVEGDLSSPEASPTAKPTAVPVKESDDKPTHEYELLW 169
Db 367 DQVRHLVRRFTARANKVKRSI---ELPPTSSSTSVSPPTKSLHSP-QH----- 416
Qy 190 FKVKKMPLEVLKRIKL-----PNSIDSYTD---RLYLLMLLVTLA 228
Db 417 -KVLVFPAGQPHGRULFEADTPRSNWLSSLCGANDBERTLDPQKIVISLVCVVSLS 475
Qy 229 YNNWCWFIPLRLVFPYQTADNIHYWLIADICDIYLYDMLFTQPLQFVRGGDIIVDSN 288
Db 476 FLYNAWVPLRASFPQTKEKNTIWLACDFCADIYLYDMLVFFKRVWYLFEGFWKKN 535
Qy 289 ELRKHYSITKFDLVASIIPIFDICILYFFGFNMP-PANRMLKYTSFFENHLESIMDK 347
Db 536 LTRKXMYRKLQFKLDLALLLELLPFLKLTQAVMLRFPFPFKIQSFWEVRLDRVSS 595
Qy 348 AYIYRVIRTTGYLLFILHINACVYVWASNYEGICTRWYVDGEGNEYLRYVWAVRTLI 407
Db 596 PHFVRVAKTLTYMLYMIHITAAIYAYSDYQGLQGNWVFGKGHVPVRCFAATKATS 655
Qy 408 IGLPPEQTLFEIVQQLNFFSGVYFVPSLIQQRVDVIGATANQNVFRACMDTTAYMN 467
Db 656 IGKPKPERQGEYVFMVAVMLMGVVFALLIGQIRDIISTATNKHGYRQLEETLEYMR 715
Qy 468 NYSIPKLVQKVRVTWYBYTWDOSRMDESLLKTLPTTVOLALADVNFISIISKVDLFG 527
Db 716 RLNLSEVQSRVXWFOFTWEQRTLDSENLALPILNKTDIAISVHICTLSKVQLFAD 775
Qy 528 CDTQMIYDMLRLKSLVYLPDGFVCKKGIGKEMVYIKHGEVQVGLGPDGTKVLTLAG 587
Db 776 CEEALLRDLVRLRAVTFPLDGFVCRKGEVREMYIKLQGVQVMGSPSSDVVYLAITEG 835
Qy 588 SVFGEISLLAAGGNNRTANVAHGPNLTLTKTQLQEILVHYPDSERILMKKARVLL- 646
Db 836 SVFGEISLLGNGADRTADVRSKGSNLFVLSKSLNEVIAIYPTAQILKGRQLMR 895

647 KQAKTATATPRKDLAL-----LFPKK--EETPKLTKLLGGTGKASLAEKLLKKEQA 699
896 KNAAREEEREERARSALQADVIGNPKTPTAPKLLQTVIALPFPSPAVLLITRSKR 955
700 AOKKENS 706
956 MRKQOS 962
PRELIMINARY; PRT; 1040 AA.
Q8IH43
ID Q8IH43
AC Q8IH43
DT 01-WAR-2003 (TREMELrel. 23, Created)
DT 01-WAR-2003 (TREMELrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE GH25102P.
GN CG17922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesen D., Farfan D., Frise E.,
RA George M., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo K., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT001439; AAN71194.1; -.
DR FlyBase; FBgn0034656; CG17922.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; CNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel pore.
DR Pfam; PF00027; CNMP binding; 1.
DR Pfam; PF00520; ion trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP BINDING_1; 1.
DR PROSITE; PS00889; CNMP BINDING_2; 1.
DR PROSITE; PS00892; CNMP BINDING_3; 1.
DR PROSITE; PS00042; CNMP BINDING; 1.
SQ SEQUENCE 1040 AA; 118713 MW; 4A643FDA21D2D5B8 CRC64;
Query Match 26.1%; Score 1103; DB 5; Length 1040;
Best Local Similarity 33.4%; Pred. No. 1.2e-68;
Matches 243; Conservative 153; Mismatches 255; Indels 76; Gaps 13;
QY 16 ENNEOSSRRNEGSHPSNQOQTAAQ-----ENKGEKSLKTKSTPVTSEPTWNI 69
DB 279 EEEEEKSSPLHQVESQPDVDEQDVQICYNESPELQNEEDRERTQRTPSINESIVAV 338
QY 70 QDKLSKKNSGDLTTPDQNAEPTGTVPQEKEMDPGKGPNSQNKPPAPVINEYAD 129
DB 339 DEPTENMSVDV---HRKPSSA---GSLDSQGG-----QFLR 369
QY 130 AQLNLVKRMQRALYKKLVGDLSSPEASQCTAKPTAVPPVKSDDKKPTSHVYVLLW 189
DB 370 DQVRHLVRRFTARANKVKSRI---ELPPTPSSSTVSSPPPTKSLHPSG-OH----- 419
QY 190 FKVKKMPLELYKRIKL-----PNSIDSYTD---RLYLLMLLLVTLA 228
DB 420 -KVLVFAQSGPHRGLFEADTPRSNWLCSLLCGANNDETLDPQCKIYISMLCVVSL 478
QY 229 YNWNCFIPLVLPFYQYADNIHNYWLIADIICDIYLYDMLFTQPLQFVRGGDIIVDSN 288

479 FLYNAWVILRASFPQTQKENTNINWACDFCADIIYLLDVFVKHVMYLFEGFWKKN 538
289 ELKHKVTRTKFOLDVASIIPFDICVLPFGFPMF-RANRMLKYTSFFFNHHLBSIMDK 347
539 LTRKNYRKLOFKLDLALLLELLYKLGTOQAVMLRPFPRFKIQSEWVFRLLDRVISS 598
348 AYIYRVIRTTGYLLFILHINACVYWNASVYEGITRWTVDGEGEYLCYKVAWVTLIT 407
599 PHEVRVAKTLTYMLYMIHITAALYYAYSQYQIGQNRWVFGKGGHPYVRCFAFATKATS 658
408 IGLPEPOTLFEIVFQLLNFFSGVFFVSSILIGOMRDVIGAAATANQNYFRACMDDTIAYVN 467
659 IGKNPPEROGEYVFTVAVLMGVFVALLIGQIRDIISTATNKHEYRQLEDETELEYMR 718
468 NYSIPKLVQKRVTRYEYTWDSQRMILDESLLKTLPTTTLVOLAIAIDVNSIISKVLFKG 527
719 RLNLSEQVQSRVQWVQFTWEQQRTLDSENLDPALPINKTKTDIAISVHIQTLSSKVLQFAD 778
528 CDQMIYDMLLRKSLVLYLPGDFVCKGGEIKGEMWIKHGEVQVVGSPDCTKVLVTLKAG 587
779 CEEALLRDLVKURAVTFLPGDFVCRKGEVREMYIVKLGQVQVMGSPSSDVVLAITLLEG 838
588 SVFGEISLLAAGGGRNRTANVAHFANLLTLDKTLQELVHYHPDSEIRILMKARVLL- 646
839 SVFGEISLLGINGADRETADVRSKGSNLFVLSKSLDNEVIAYVPTAAKILKRRAROLMR 898
647 KQAKTATATPRKDLAL-----LFPKK--EETPKLTKLLGGTGKASLAEKLLKKEQA 699
896 KNAAREEEREERARSALQADVIGNPKTPTAPKLLQTVIALPFPSPAVLLITRSKR 955
700 AOKKENS 706
956 MRKQOS 962
PRELIMINARY; PRT; 800 AA.
P90975
ID P90975
AC P90975
DT 01-MAY-1997 (TREMELrel. 03, Created)
DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cyclic nucleotide-gated channel.
GN P36P2.5 OR TAX-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97048185; PubMed=8893026;
RA Coburn C.M., Bargmann C.I.;
RT "A putative cyclic nucleotide-gated channel is required for sensory
development and function in C. elegans.";
RL Neuron 17:695-706(1996).
DR EMBL; U73476; AAB41492.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; CNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel pore.
DR InterPro; IPR001202; WW_Rsp5 WWP.
DR Pfam; PF00027; CNMP binding; 1.
DR Pfam; PF00520; ion trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP BINDING_1; 1.
DR PROSITE; PS00889; CNMP BINDING_2; 1.
DR PROSITE; PS00042; CNMP BINDING_3; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 1.

```

KW Ionic channel; Transmembrane.
SQ SEQUENCE 800 AA; 92462 MW; D0498AD2C340FDAA CRC64;

Query Match 25.9%; Score 1096; DB 5; Length 800;
Best Local Similarity 31.5%; Pred. No. 2.5e-68;
Matches 253; Conservative 146; Mismatches 301; Indels 102; Gaps 19;

QY 26 RNEGSHPSNQSQQTTAAQENKG-----EESKLTKSTPTVTSSEFHTNIQDKLSKXSSG 80
Db 17 RKREFSYVDROKASKPTQLSEKWKSPRESDSFLLDPANASKEP----- 61
QY 81 DLTTNPPQNAAP-----TGTVPQKE-----VDPKGEPSNPKNPPA 120
Db 62 SASRPLPYPTRPPEVVIQIDEVESFILGLIDETDDELDGRDPASSFDANSLSATRA 121
QY 121 APVINEYADAQ-----LHNLVKRMQRQALYKKKLVEGDLSSPEASPOAKPTAVPP 172
Db 122 SSIIEDVRSQISFIMRERLHSAKEVHRTSAVREDLIR---ETPEDTYSMA--SNVP- 175
QY 173 VKESDDKPTHEYHLLMKPKVK-KMPLTEYIKR---IKLPNSIDSYTDRLYLLMLLVTLA 228
Db 176 -KQNEHRS--LMSLIGLQNRSESPSTDVTKNCGFSLKGTFFPY-GRFYMTLWLSVTL 231
QY 229 YNNMCWPIRLRVFPYQADNIHWLMTADIICDIYLYDMLFTQPRLOFVRGGDIIVDSN 298
Db 232 FLNFAFCIPLRSSPYQADNMWFIIVDYSCLVYVYIDMLLKPRLFRTRGGIQKIYK 291
QY 289 ELKHYRTSTKFOJDVASIIPFICYLFFGFNPMFRANMLKYTSPFEFNHLESIMDKA 348
Db 292 DTQRHYLWMTRFKLDLSILPTDLYTFFFCMPINRNLKINSFWLLFMDLNDSFANP 351
QY 349 YIVRVITTCYLLFILHINACTVYMASNYEGIG-----TTRWYVDGEGNYLRC 397
Db 352 YAIRIARTLSYMIYTHCNSCVYKLSALQAFQIAYLENGKYLKNKVVYNNQGNAYIRC 411
QY 398 YWAVRPLTIIGGLPEPQTFEIVFOLLNPFSGVVFSSLIGOMRDVIGAAATANYERA 457
Db 412 FYTAAVATSTGNPAPTNVIEIYVTCSSWNGVVFALLGGQIRDIVSVANRNEEOR 471
QY 458 CMDTDTAYMNNYSIPKLVQKRVTWZEYTWDSQRMLEDSDLLKTLPTTVQLALADVNF 517
Db 472 KMDLALGECKKLGLKMETTNVRDWFYTWQQOKTLDKGLIEKLPLKQLDLSVHVT 531
QY 518 IISKVDLPKCDTQMLYDMLLRKLSVLYLPDGPVCKKGIGKEMYIIKGEVQVLTGGPG 577
Db 532 TLSKVQJFOCDRALLURDLVKLRPIFIPGDMICLKGDVGKEMYIIINGQILQWGDHN 591
QY 578 TKVLTVLKAGSVEGISLLAAGGNRRRTANVAHGFANLLTLDKKTQLBILVHYPDSE 637
Db 592 EKIFAEALQAGVGEISLLAIGNNRRTASIRAKGYCTTLFVLAKEDLNDVIRYVPOAQ 651
QY 638 LMKARVLLKQAKTABEATFPKDLALL-----FPPKEETPKLFTLLGGT-----GKA 686
Db 652 LRRKAAMLKNDKKSDEKTEKIAQAELEDRCINKINP-QVPKLITLIANNTEMNENKVG 710
QY 687 SLARLLKLRQAAQKK-----ENSEGGEEGEKENEDKOKENED-----KOKENED 732
Db 711 ELKVLIEETEKSRRSQSIYYPNASTLQRDDDDDEEWNDEEDLSDVGEDFDLPDNTNHSDD 770
QY 733 KOKENEDKQGREPPEKPLDRP 754
Db 771 ---PMEDVDLAPVEVHDDWDQ 789

```

Search completed: June 21, 2004, 10:07:18
Job time : 57 secs


```

Db 477 GSTHWVGVGNSYRIRYFAVKTLITIGLPDPKTLFEIIVFQLLNYFTGVFAFVMIQ 536
QY 441 MRDVI GAATANQYPRACMDDTIANNYSIPKLVQKRVRTWYBYTWDQSQMLDESLLK 500
Db 537 MRDVVGAATAGQTYRSCWDSVTVMNFYKIPKSVQNRVKTWYBYTWHSQMLDESILMV 596
QY 501 TLPTTVQALALADNVFSLISKVDLPFGCDTOMIVDMLRLKSLVLYLPDGFVCKRGEIGKE 560
Db 597 QLPDQMRDLDAIDVNNIVSKVALFQGCDDQWIFDMLKRLSVLYLPNDYVCKRGEIGRE 656
QY 561 MYIIKHGEVQVLGPDGKVLVTLKAGSVFGEISLLAAGGNNRRRTANVAHGFANLITLD 620
Db 657 MYIIQAGVQVLGPDGKSLVTLKAGSVFGEISLLAAGGNNRRRTANVAHGFANLITLD 716
QY 621 KKTLOSILVHPDSEIRILMKARVLLKQAKTAETAPRKDLALIFPKKETPKLKTLL 680
Db 717 KKDLEILVHPDSEIRILMKARVLLKQAKTAETAPRKDLALIFPKKETPKLKTLL 771
QY 681 GGTGRAS-----LALLKLKREQAQKENSEGEGEKEGKEDKQK 728
Db 772 AMTGRWGGKAGGKLALHARLRLKELALEAAKQOEL---VEQAKSSQDVKGEGSAAP 828
QY 729 ENEDKGKE-NEDXKGRPEKPP-----LDRPECTASPIAVEEPHPSVRTVLP 776
Db 829 DQHTHPKEAATDPPAPRTPPEPPGSPSPSPASLGRPEGEEGPA-EPEEHSVR----- 882
QY 777 RGTSRQSLIISMAPSAGGEEVLTIEVKEKAK 809
Db 883 -----ICMSPGPEGEQILSVKMPERE 906

RESULT 2
T19627
Hypothetical protein F36F2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T19627; 121863
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19627
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-800 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CA807847.1; GSPDB:GN00019; CESP:F36F2.5
A:Experimental source: clone C31H5
R:Cottage, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19479
A:Accession: T21863
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-800 <W12>
A:Cross-references: EMBL:Z81532; PIDN:CA804328.1; GSPDB:GN00019; CESP:F36F2.5
A:Experimental source: clone F36F2
C:Genetics:
A:Gene: CESP:F36F2.5
A:Map position: 1
A:Introns: 27/3; 51/2; 142/2; 191/3; 287/3; 333/3; 355/2; 405/1; 433/2; 484/1; 508/1; 56
Query Match 25.9%; Score 1095; DB 2; Length 800;
Best Local Similarity 31.9%; Pred. No. 1.9e-59;
Matches 258; Conservative 153; Mismatches 301; Indels 98; Gaps 22;
QY 2 FKSLLTKNVKVRPIGENNENESSRNEG-----SHPSVQSQTAAQENKGEESLTKYST 58
Db 21 FSYVDQRQKASRPT-QLSEKWKSPRSDSPDLLDPANAS-----KEPSASTRPL 68
QY 59 PV-TSEEPHTNIQDKLSKNSGDIITNP-----DPQNAAEPTGTVPQEMDPGKEGPN 112
Db 69 PYPTRPRPEVVIQI-----DEVESPIGLIDETDDHLDG-----RLDPASSFDA 113
QY 113 SPQNKPPAAPVINEYADAQ-----LHNLVKRMRORTALYKKKLVGDLSSPEASPT 164

```

```

Db 114 NSLSATRASIIEDDVRSQISFIMBERLHSAKEVHRRTSAVREDLIR---ETPDTVSM 170
QY 165 AKPTAVPPVKESDDKPTHEYHLLMFKVK-KMPLTEYLKR---IKLPNSIDSYDRLLYL 220
Db 171 A--SNVP--KQNEHRPS--LMSLIGLQNRSEPTVDTKNCFGSLKGTFFPY-GRFYMT 223
QY 221 WLLVTLAYNNWCMTPIRLVFPYOTADNIHYNLADIICDIILYDMLFTQPRLOFVRG 280
Db 224 WLSVTLCLFNAFCPLRSSYPQYADNMWTFWIDYSCDLYVIDMLLKPRKFRTRG 283
QY 281 GDIIVDSNELRKHRTSTRTKFQDVASIIIPDFICYLFGFNPMPFRANRMLKTSFFEFNH 340
Db 284 GIQVKIYKDTQRHYLMWTRTFKLDLSILPTDLMYFFFGKPIWRINRVLKINSFWLLPDM 343
QY 341 LBSIMDKAIYIVRTTGYLLFILHINACVYVWASNYEGIG-----TTWVYDG 389
Db 344 LNSFANPAIRIARTLSYMIYIIHCNSCVYKLSALQAFQGIAYLENGKWLKNWVYNN 403
QY 390 EGNELRCYVWAVRTLITIGLPEPQTLEIIVFQLLNFFSGVVFSSLIQMRDVIGAT 449
Db 404 QGNAYIRCFYFTAATVATSGNNPAPTNIYEVYMTCSWMMGVFVALLGQIRDIVSNAN 463
QY 450 ANQNYPRACMDDTIANNYSIPKLVQKRVRTWYBYTWDQSQMLDESLLKTLPTVOLA 509
Db 464 RNREEFORQMDLALGCECKLGLKMETTNVRDMFTYTQOQKTLDEKLEIKLPLQTD 523
QY 510 LAIDVNFSLISKVDLPFGCDTOMIVDMLRLKSLVLYLPDGFVCKRGEIGKEV 569
Db 524 LALSVMHTLSKVQLFQDCDRALLDLVLKLPVLPFGDMCLKSGDVKEMVINQOIL 583
QY 570 QVLGGPDGKVLVTLKAGSVFGEISLLAAGGNNRRRTANVAHGFANLITLTKTLQELIV 629
Db 584 QVVGSDHNEKIFAELAQGAVFGEISLLAAGGNNRRRTASTIRAKGYCTLFVLAKEDLNDVIR 643
QY 630 HYPDSERILMKARVLLKQAKTAETAPRKDLALL-----PPKPEETPKLTKLGGT- 683
Db 644 YYPQAOITLIRRAAAWLVKDKSKDEKTEKIKQAQAELEDRCKINPR-QVPKLITLITANWTE 702
QY 684 -----GKASLARILKLKREQAQK-----ENSEGEEGKEGKEDKQKED- 725
Db 703 MNENKGVQELKKVIBETEKSRRQIYVYVSWTSLQDDDDDEEWNDEEDLSVGDGFDLDP 762
QY 726 -KQENEDKGENEDKDKRPEPEKPLDRP 754
Db 763 TNHSDDED---PMEDVDLAPEVHDDDDQDP 789

RESULT 3
S74179
Cyclic nucleotide-gated channel protein - human
C:Species: Homo sapiens (man)
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999
C:Accession: S74179
R:Yu, W.P.; Grunwald, M.E.; Yau, K.W.
FEBS Lett. 393, 211-215, 1996
A:Title: Molecular cloning, functional expression and chromosomal localization of a human
A:Reference number: S74179; MUID:96409310; PMID:8814292
A:Accession: S74179
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-695 <YUW>
A:Experimental source: retina
C:Genetics:
A:Superfamily: 2
A:Map position: 2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: ion channel; ion transport; membrane protein
F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 19.7%; Score 834.5; DB 2; Length 695;
Best Local Similarity 29.7%; Pred. No. 1.5e-43;
Matches 223; Conservative 149; Mismatches 271; Indels 107; Gaps 22;

```

Qy	27	NEBGSHPNSOQQTAAQENKGEBSLTKSTPVTSEBPHNTIQDKLSKNNSCDLITNP	86
Db	5	NTQYSHPS-----RTHLEKVTSDRDLNRAENGLSRAHSSEETS--	43
Qy	87	DPONAAEPTGTVPBOKEMDPCKECPNSPQNKPPAAPVINEYADAQALHNIVKRNQRTALY	146
Db	44	---SVLQP-GIAMETRGLADSGGGSFTGQ-----GIARLSRLIFILRRWAARH	87
Qy	147	KKKLVBGDLSP-----EASPTAKTATVPVPKESDDKPTHEYHRLWFKVKMPL	197
Db	88	VHHQDQDPSFDPFRGAELKEVSSQESNAQANVGQEPADRG-----ESAW-----PL	136
Qy	198	-----TEYLKRIKLPSNI-DSVTDLYLLWLLVTLAYNWNWCWFIPLRLVPYQT	246
Db	137	AKCNTNTSNITEBEKTKKDAIVDPSNNLYVRWLTALVPVFNWYLLICRACFDELQ	196
Qy	247	ADNIHYWLIADIICDIIVLYDMLPIQRPLOFVRGGDIIVDSNELRKHRYTSTKFQLDVAS	306
Db	197	SEVLMMLVLVDYSADVLVLDVL-VRAARTGFLBQGLMSDTNRLWQHYTKTTFKLDVLS	255
Qy	307	IIPEDICVLPFGFN-PMFRANRMLKYTSFEFNHHLSESIMDKAYIVRVIRTTGYLLFILH	365
Db	256	LVPTDLYLKVGTNYPEVRFNRLKPSRLFEFFDRETETRTNYPNMFIGNLVLYLIIH	315
Qy	366	INACVYWASNYEGIGTRWYDQ-----BONEYLCYCYWAVRTLTITIGGLPEPQTL	417
Db	316	WNACIYPAISKFIFGFGTDSWYPYNISIPERGLRSKRYISLYMSTLTLTITIGTTPPVKD	375
Qy	418	PEIVFOLLNPFSGVVFVSSLLIGOMRDVIGAATANCONFRACMDDTIAYMNNYSIPKLVOX	477
Db	376	EYLFVVVDVFLVGLVLIITATIVGNVGSIMSNWASRAEFOAKIDSIKQYMFVKVKDLET	435
Qy	478	RVRTWYBTWDSQRMLESDDLKTLPTTVQLALADIVNFSIISKVLKFGCDTQMYYDML	537
Db	436	RVIRWFYLVANKNTVDEKEVLKSLPKLKAETAINVHLDTLTKVRIFOCEAGLIVELY	495
Qy	538	LRLXSVLVLPDGFVCKKGEIKGEWYIILKHGBQVLGGPDGTFKVLTVLUKAGSVFGEISLLA	597
Db	496	LKLRPTVPSPGDYICKKGIDIGEKWYIINEGKLVV-ADDGVTQFVVLSDGSYFGEISILN	554
Qy	598	AGG---GNRRNTANYVAHGFANLLTLDKKTLOEILVHYIP-DSEIRILMKAR-VLTKQK---	649
Db	555	IKGSKSGNRRNTANIRSIGYSFLFCLSKODLMEALTEYPGOAKKALBEKGRQILMKONLID	614
Qy	650	AKTAEATPPKDLALLPPPKETPKLTKTLGGTGKASLARLL-----KLKREOAAQ	701
Db	615	EELARAGADPKDL-----EBKVQLGSSL-DTLOTRFAKLLAEYVATQWKKQRLSQL	666
Qy	702	KKENSEGEE---EGKENEDKQENEDKQK	728
Db	667	ESOVKGGDKPLADGEVPGDATK-TEDKQO	695

RESULT 4

S11521
cAMP-gated channel protein - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S11521
R:Ludwig, J.; Margalit, T.; Eismann, E.; Lancet, D.; Kaupp, U.B.
PDBS Lett. 270, 24-29, 1990
A:Title: Primary structure of cAMP-gated channel from bovine olfactory epithelium.
A:Reference number: S11521; MUID:91032022; PMID:1699793
A:Accession: S11521
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-663 <LDD>
A:Cross-references: G3:X55010; NID:G287743; PIDN:CAA38754.1; PID:G287744
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
F:454-578/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.6%; Score 829; DB 2; Length 663;
Best Local Similarity 29.9%; Pred. No. 3.1e-43;

Matches	218;	Conservative	132;	Mismatches	283;	Indels	96;	Gaps	20;
Qy	50	EKSILKTSPTVTSEEPHTNIQDKLSKQSSGDLTTPDPQNA--EPTGTVPEQKEMDPG	107						
Dd	3	EKANGVKKSSPANNHNHAPPAIKASGD---DHRASGRPQSAADDDTSEUQQLAEMDAP	59						
Qy	108	KEGPNSPONKPPAAPVINEVA-----DAQHLVLKMRQRTALYKKKLVEGDLSSPA	160						
Dd	60	QQRGGGPRFARLVGLVREWAYRNFRBEEPRPDSFLERF-----GPEL	103						
Qy	161	SPOTAKTAVPPVKESDDKPTHEYHYRLLVFKVKMPLTEYLKRIKLPSIDSYTDRLLYLL	220						
Dd	104	HTVTTQGGDKGDKGEGKGTGKKFELF-----VLDPAGD-WYR	142						
Qy	221	WLLLVTL--AYNNMCWPIPLRLVPEPYQTADNIHWLIADIICDIIYLYDMLFIQRLQFV	278						
Dd	143	WLFIALLPVLYNW-CLLV-ARACSDIQLKGYIVWLVLVDYSDVVIAD-LFIRLTGFL	199						
Qy	279	RGDIIVDSNELRKHYTSTKFDQDVASIIIPDCYLFEGF-NPMFRANRMUKIYTSFFPF	337						
Dd	200	EQGLLVKDTTKLRNYIHTMFKLDVASIIPDLYFAVGHNPEVRFNRLLHFARMFEP	259						
Qy	338	NHLESIMDKAYIVRVIRTTGTYLLFILHINACVYVWASNYEGIGTRWVY-----DGE---	390						
Dd	260	FDRTEITSYPIFRISNLIIYIIIIHNACIYVAISKSIGFGVDTWYVPIITDEYGY	319						
Qy	391	-GNEYLRCYWAVETLITIGSLPBPQTLFEIVQQLNPFSGVVFSSLIQMRDVIKAAT	449						
Dd	320	LSREYIYCLYWSTLTLTITGTPTPPVKDEEYLFVDFLIGVLIFATIVGNVGSIMSNMN	379						
Qy	450	ANQVYFACDDDTIAYNNYISIPKIVQKRVRTWYETWDSORMLDESLLKTLPTTVQLA	509						
Dd	380	ATRAEPQAKDAVGHYVQFVKVSKEMEAKVIRWFYLTWTKASVDEREVLKLPKALRAE	439						
Qy	510	LADVNFISIISKVDLFGCDTQMTYDMLRLKSVLYLPDGFVKKGKGEIKEMYIIKHGEV	569						
Dd	440	IAINVHLSTLKKVIRIFQDCEAGLIVELVCLKRPQVFPQGYICRKGDIGKEMYIIKEGL	499						
Qy	570	QVLGGPDGTVLVLIKAGSVFGEISLLAAG---GNERTANVVAHGAFANLLTLDKTLQF	626						
Dd	500	AVV-ADGVTVQYALLSAGSCFGEISILKSGKGNRRRTANIRSGISDLFCLSKDDLME	558						
Qy	627	ILVHYPDSERILMKKARVLLKQAKTAE---ATPPRKDALALPPPKBETPKFKTLGGT	683						
Dd	559	AVTEYPPDAKRVLESRGRILMKEGLLDNEVAASMEVDV-----QEKLEQLETNN--DT	610						
Qy	684	GKASLARILLKLRQAQAKKENSEGEGEKENEDKOKEN--EDKOKENEDKGENEDKD	741						
Dd	611	LYTRFARLL-----AETGAQCKLKQRIIVLETKMKQNNEDDSLSDGWN	654						
Qy	742	KGREPEEKP	750						
Dd	655	SPEPPAEKP	663						
RESULT	5								
	150630	alpha subunit of cone photoreceptor CNG-channel - chicken							
	C:Species: Gallus Gallus (chicken)								
	C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999								
	C:Accession: U50630								
	R:Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Moiday, R.S.; Kaupp, U.B.								
	Neuron 10, 865-877, 1993								
	A:Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels								
	A:Reference number: U50630; PMID:93264082; PMID:7684234								

RESULT 5
150630
alpha subunit of cone photoreceptor CNG-channel - chicken
C:Species: Gallus Gallus (Chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: 150630
F:Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B
Neuron 10, 865-877, 1993
A:Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
A:Reference number: 150630; MUID:93264082; PMID:7684234
A:Accession: 150630
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A. Residues: 1-735 <BON>
A. Cross-references: ENML:X89598; NID:G908950; PID:CA61757.1; PID:G908851
C. Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:524-648/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>


```

Db      3  LSKMTNIINTWHSFVNI PNVIIPATEIKELRRMENGACSFSDDDN-----GSLSESENE 57
Qy      106 PG-----KEGNSPQNKPAAPV---INAYADAQLHNLVKRMQRORTALYKKKLVEGD 154
Db      58  DSFFRSNYSKRSGPSREQHLEGTWALFNWNSSNKDQEPKEKKKKK-----EKSKKADD 113
Qy      155 LSPSEASPOKAPTAAPVPKESDQKTEHYRLLWFKVKMPLTEYLKRIKLPNSIDSYT 214
Db      114 KENKDKPEKKKKE-----KEKEKKKE-----KTEKEEBEKKVVDPSGNTVY 162
Qy      215 DRLLYLWLLLVTL--AYNNCWPIRLVPPVQTADNIHLYLADIICDIIYLYDMFLQ 272
Db      163 N-----WLFCTILPVNMYNT--MIIARACFDELQSDYLEWLFIDYVSNVYLADM-FVR 214
Qy      273 PRLQFVRGGDIIVDSNELKRYRTSKFOLDVASIIPFDICYLFFGFN-PMFRANRMLKY 331
Db      215 TRTGYLEQGLVQKDRWKLIEKYKANLOPKLDVLSVPTDLLYIKFGWNYPEIRLNELLRI 274
Qy      332 TSPFEFNHLESIMDKAYIRVIRTGGYLLFILHINACVYVWASNYEGIGTRWVY----387
Db      275 SRMFEFFQRTETRTNYPNIFRISNLVMYIVIIHWNACVYSISKALGFNDTWVYPDVN 334
Qy      388 DGE-----GNEYLYRCYKAVRTLTIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQOMED 443
Db      335 DPFGRLARKYVSLXWSTLTLTIGETPPVLDSEYFVVDVFLIGVLIFATIVGNIGS 394
Qy      444 VIGAATANQNYFRACDDMTIAYNNYSIPKLQKRVRTWYETWDSQRMLEDSDLLKTLIP 503
Db      395 MISNMNAARAEFOSRDVAIKQYFNFRNVSKDMKRVLKWFDYLTWNTKTVDEREVLRYLP 454
Qy      504 TTVOLALADNFSIISKVDLFGKCDTQMIYDMLRLKSVLYLPGDFVCKKGIGKEMVI 563
Db      455 DKLRAETAINVHLDLTKKVRIFADCEAGLLVELVLQPOVSPGDYICKGDIKREMYI 514
Qy      564 IKHGEVOVLGGPGDGTKVLYLTKAGSVFGEISLLAAGG---GNERTANVAHGPFANLLTLD 620
Db      515 IKEGKLVV-ADGIGTQFVVLSDGSGEISILNIGSKAGNRTANIKSIGVSDLFCLSL 573
Qy      621 KKTLEILVHYPPSERILMKARVLL 646
Db      574 KODLMEVLTEYDPAKTMLEBKRGQIL 599

RESULT 8
A42161
CGMP-gated cation channel, rod photoreceptor - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
C:Accession: A42161
R:Pittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; Wa
J. Biol. Chem. 267, 6257-6262, 1992
A:Title: Primary structure and chromosomal localization of human and mouse rod photorece
A:Reference number: A42161; MUID:92210603; PMID:1372902
C:Accession: A42161
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-690 <PT>
A:Cross-references: GB:M84741; NID:G180461; PIDN:AAA52010.1; PID:G180462
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cAMP binding; transmembrane protein
F:479-603/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match      19.3%; Score 818.5; DB 2; Length 690;
Best Local Similarity 30.0%; Pred. No. 1.5e-42;
Matches 221; Conservative 128; Mismatches 262; Indels 125; Gaps 22;

Qy      5  LTKVNVKPIGNNENEGSSRRNEGSHPS-----NQSQQTAAQENKGE-----KSL 53
Db      17  VTMPNVIVP-----DIEKEIRRMENGACSFSDDDSGAYTSESEENPHARGSFYSKSL 71
Qy      54  KTKSTPTVSEPHNTIQDKLSKSSGDLTTNPPQNAABPTGVTPQKEMDPCKEGPNS 113
Db      72  R-KGGSQREQVLPGAIAIFNVNNS-----NKO-----QEPPEKKKKKKKKSKSDKNE 121

```

```

Qy      114  POKPPAAPVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSPSEASPOKAPTAAPVP 173
Db      122  NKNDPE-----KKKKKDKKKKK-----E 141
Qy      174  KESDDKTEHYRLLWFKVKMPLTEYLKRIKLPNSIDSYTDRLLYLWLLLVTL--AYNW 231
Db      142  EKSXDKKEHH-----KKEVVV-----IDP-SGNTYYNWLFCITILPVNMYNW 180
Qy      232  NCWFIPRLVFPVQYADNIHLYLADIICDIIYLYDMFLQIPRLQFVRGGDIIVDSNELR 291
Db      181  T--WVIARACFDELQSDYLEWLFIDYVSDIVYLDIM-FVTRTRTGYLEQGLLVKEELKI 237
Qy      292  KHYTSTKFDLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFPEFNHLESIMDKAYI 350
Db      238  NKYKSNLOPKLDVLSIPTDLLYFKLGWNYPEIRLNELLRFRSMFPEFFQRTETRTNYPNI 297
Qy      351  YRVIRTTGTYLLFILHINACVYVWASNYEGIGTRWVY-----DGE-----GNEYLYRCYVWAV 402
Db      298  FRISNLVMYIVIIHWNACVYSISKALGFNDTWVYPDINDPFGRLARKYVVSILYWS 357
Qy      403  RTLITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQOMRDVIGAAATANQNYFRACDDMT 462
Db      358  LTLTIGETPPVLDSEYFVVDVFLIGVLIFATIVGNIGSMISNMNAARAEFQARIDAI 417
Qy      463  IAYNNYSIPKLQKRVRTWYETWDSQRMLEDSDLLKTLPTTVQLALAIQVNFSSIISKV 522
Db      418  KOYMEFRNVSKDMKRVLKWFDYLTWNTKTVDEKEVLKYLDPKRAETAINVHLDLTKV 477
Qy      523  DLFGKCDTQMIYDMLRLKSVLYLPGDFVCKKGIGKEMVI--IKHGEVOVLGGPGDGTKVLY 582
Db      478  RIFADCEAGLLVELVLQPOVSPGDYICKGDIKREMYI--IKGKLVV-ADGIGTQFV 536
Qy      583  TLKAGSVFGEISLLAAGG---GNERTANVAHGPFANLLTLDKKTQELIVHYPPSERILM 639
Db      537  VLSDGSTGGEISILNIGSKAGNRTANIKSIGVSDLFCLSKDDLMLEALTEYDPAKTMLE 596
Qy      640  KKAARVLLKQKA---KTAETATPPRKDLALLPFPKPEETPKLFKTLGGTGKASLAE 692
Db      597  EKGKQILMKDGLDLNLANAGSDPKLEEKVTRMEGSDVLLQT-----RFAIILAEY 648
Qy      693  -----KLKREOAAQKK 703
Db      649  ESMQOKLAKRLTKVKEK 664

RESULT 9
A44842
CGMP-Gated ion channel protein - human
N:Alternate names: rod photoreceptor cGMP-gated channel
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A44842
R:Dhallan, R.S.; Macke, J.P.; Eddy, R.L.; Shows, T.B.; Reed, R.R.; Yau, K.W.; Nathans, J
J. Neurosci. 12, 3248-3256, 1992
A:Title: Human rod photoreceptor cGMP-gated channel: amino acid sequence, gene structure,
A:Reference number: A44842; MUID:92356211; PMID:1379636
A:Accession: A44842
A:Molecule type: mRNA
A:Residues: 1-666 <DHA>
A:Cross-references: GB:S42457; NID:G252853; PIDN:AAE22778.1; PID:G252854
A:Experimental source: retina
A:Note: sequence extracted from NCBI backbone (NCBI:110250, NCBI:110251)
C:Genetics:
A:Gene: GDB:CNCG1: CNCG
A:Cross-references: GDB:127557; OMIM:123825
A:Map position: 4p14-4q13
A:Introns: 36/2; 75/2; 95/2; 110/2; 146/2; 182/2; 218/2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cAMP binding; eye; ion channel; ion transport; retina; transmembrane protein
F:475-599/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

```

```

Query Match      19.3%; Score 818; DB 1; Length 686;
Best Local Similarity 29.9%; Pred. No. 1.6e-42;
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

Qy 5 LTKYKVKPIGENNENEGSSRRNEGSHPS-----NQSOQTTAQENKGE-----KSL 53
Db 13 VIMPNVIVP-----DIEKEIIRMENGACSSPEDDDSSASTSEENENPHARGSFYSKSL 67
Qy 54 KTKSTPVTSSEPHNTIODKLSKQSSGDLTNPDPQNAABPTGTVPEOKEMDPGKEGPN 113
Db 68 R-KGSPSREQYLPGAIALFVNWSS-----NKD-----QEPEKKKKKKKSKDNKVE 117
Qy 114 PONTXPPAPVINEVADAQLNLVFRMORTALYKXKLVEGLDSEPAEPQAKTAVPPV 173
Db 118 NKNDPE-----KKKKKKKKKK-----E 137
Qy 174 KESDDKPTHEYRYLLWFKVKWMPTEYLKRIKLPNSIDSVTRDLYLLWLLAVL--AYNW 231
Db 138 ESKDKKXEEE-----KEVV-----IDP-SCNTYYNWLFCTILFVWYNW 176
Qy 232 NCWFIPRLRPVYOTADNIHWIADIICDIYIYDMLFIQPRLOQVRGSDIIVDSNELR 291
Db 177 T--MVIARACDELQSDYLEWILDYVSDIVYLDI--FVTRTRTGYLEQGLLVKEELKI 233
Qy 292 KHYTSKFKOLDVASIIPFDICLYFFGFN--PMFANRMLKXTSFEFNHLESIMDKAYI 350
Db 234 NKYSNTQFKLDVUSLPTDILLYPKLGWNYPEIRLNLLRFSRMFEFQFTRTNTYPI 293
Qy 351 YRVIRTTGYLLFILHINACVYVWASNYEGIGITRWVY-----DGE-----GNEYLCYVWAV 402
Db 294 FRI SNLWYIYIILHNACVYFYSISKALGFNDTWVYPDINDPEFGRLARKYVYSLWST 353
Qy 403 RLLITIGLPEPQTLFEIVPQLLNFPFGVVFSSLIQOMRDVIGAAFTANQNYFRACMDDT 462
Db 354 LTLTTIGETPPVRDSEYFVVDVFLIGLVIFATIVGNISMINNMAARAEQARIDAI 413
Qy 463 IAYMNNYSIPEKLVOKRYTWYETWDSQRMLEDSDLLKLTPTTVQLALAIADVNFISIYV 522
Db 414 KQYMHFRVSKDEKRVIKFDFLWTKTVDEKEVLKLPDKLRAEIAINVHLDTLKKV 473
Qy 523 DLFKGCOTQMIYDMLLRKLSVLYLPGDFVCKGGEIGKEMYIIKHGEVQVLGGPDGTVKLV 582
Db 474 RIFADCEAGLLVELVLKLPQVYSPGYICKGDI GREYIIKEGKLVV--ADGVTQFV 532
Qy 583 TLKAGSVFGESISLLAAG---GHRRTANVAGFANLLTDKKTQLQBILVHYDPDSERILM 639
Db 533 VLSGDSYFGEISILNTIKGSAGNRRTANIKSIGYSDLFCLSKODLMEALTEYPDATMLE 592
Qy 640 KKAIVLLKQRA---KTAETAPPRKLLALLFPKPETFKPLKTLGSGTKGASLARLL--- 692
Db 593 EKXQKILMDGLLDLNIANAGSDPKLEEKVTRMEGSDVLLQT-----RPARILAEY 644
Qy 693 -----KLKREQAQAQK-----ENSEG-GESEG 713
Db 645 ESMQCKLKQRLTKVEKFLKPLIDTEFSSIGPGAESG 681

```

RESULT 10
JH0560
Cyclic nucleotide-gated channel - channel catfish
C:Species: *Italurus punctatus* (channel catfish)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_charge 10-Sep-1999
C:Accession: JH0560
R:Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Chess
Nuron 8 45-58, 1992
A:Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
A:Reference number: JH0560; PMID:92110008; PMID:1370374
A:Accession: JH0560
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-682 <GU>
A:Cross-references: GB:M83111
A:Experimental source: olfactory epithelium

C;Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP ar
C;Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-b
C;Keywords: CAMP binding; CGMP binding; ion channel; ion transport; olfaction; transmembr
F.137-157/Domain: transmembrane #status predicted <TS1>
F.173-193/Domain: transmembrane #status predicted <TS2>
F.173-193/Domain: transmembrane #status predicted <TS2>
F.217-236/Domain: transmembrane #status predicted <TS3>
F.241-261/Domain: transmembrane #status predicted <TS4>
F.277-297/Domain: transmembrane #status predicted <TS5>
F.319-337/Domain: transmembrane #status predicted <TS5>
F.350-370/Domain: transmembrane #status predicted <TS6>
F.447-571/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match	19.1%	Score 807.5	DB 1	Length 682
Best Local Similarity	29.0%	Pred. No. 6.8e-42		
Matches 192	Conservative 137	Mismatches 256	Indels 77	Gaps 17
QY	119	PAAEVINEYAD----	AQLHLVGRMQROTALYKKVLVEGDLSSPA-----	SPTAKPT 168
Db	55	PSAEMLSAFTORRPLARLVNLVLSLEWA----	HKSIVETE-QRPDSFLFRFRGPOAANDQ 110	
QY	169	AVPVKESDDKPT-EHYVRLVFWFKVOMPLTEYKRIKLPNSIDS	YDRLYLWLLVLLVLA 228	
Db	111	SAAFA-----	DAPKTF-----	KERWEGFVVSODDIYYWVLFIALA 148
QY	229	--YNNWCWFPLRLVPFYOTADNIHWYLIADIICDI	LYLDMLFIQPRLOQVRGDIIVD 286	
Db	149	SLYNW--IMLVARACFDQLQDENFFLWVGDLVLC	DVILDTCLRLRTGVLEQGLLVKD 205	
QY	287	SNEARKHYRSTFKOLFDVASII	PPDICYLFFGFENPMFRANMLKYTSFEEFNHLESIMD 346	
Db	206	LAKLRDNYIKTLOFKLDFSI	LPTLELLFVTVGVQLFRNLLRFSRMEFPFDRTRTN 265	
QY	347	KAYIVIRITGTLLFILHINACVYVWASNYEGIGTRWY	VDGEGNE----YLCRYWAV 402	
Db	266	YPNAPRICNLILYILIIHNNACIYVASKALG	LSDTWVSGQNKTLSPCYVVCFWST 325	
QY	403	RTLITIGLPEPOTLFEIYVQLNFP	SGVVFESSLIGQMRDVIGAATANQNYFRACMDDT 462	
Db	326	LTLTTIGEMPVPKDEEYVYVWF	DLVGLVLIIPATIVGVNVMIANMNAETRAEFQTRIDAI 385	
QY	463	IAYNNVSIPLVOKEVRTWYETVWDSQRM	DESLLKTLPTTVQLALADVNSIISKV 522	
Db	386	KHYHFRKVNRTLSTRVIKWF	LYLTKNKTVDQEVLLKMLPKLRAEIAINVHDLTKKV 445	
QY	523	DLFKGCDTQMIYDMLRLKSVLYLP	GFCKVCKGEIGKEMWIIKGEVOVLGGPGDTKVLV 582	
Db	446	RIQDCENGILLVELVLKLPVQV	SGDVICRKGDIKEMWIIKESQLAVV-ADDGVTOFA 504	
QY	583	TLKAGSVFGEISLLAAG--	-GNRRTANVVAHGFANLTLTKKTLQEILVHPDSEIRLM 639	
Db	505	LTTAGGCFGEISILNIQSGKMG	NRRTANTIRSIGSDFLCLSKDLMBAVBPDAQVLE 564	
QY	640	KKARVLLKQAKTAATP-----	-----PRKDLALLFPFKETPKLFTLLG---GT 683	
Db	565	ERGRELKQGLLDSVAAGGLV	IDTBKVERLDASL-----DILQTRFARLLGEFTST 619	
QY	684	GKASLARLLKLKREQA----	AQKENSEGGEBEEG---KENEDKOKENEDKOKENEDKGE 736	
Db	620	QRRLKQRITALERQLCHTGLGL	SLDSNEAGEHAGVPTHADIIHAQPEPTHTRISAEINSE 679	
QY	737	NE 738		
Db	680	EE 681		

RESULT 11

gill17
cyclic nucleotide-activated channel protein - rat
Species: Rattus norvegicus (Norway rat)
Accession: G1117 #sequence_revision 10-Nov-1995 #ext_change 13-Aug-1999
Daallan R. S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.
Nature 347, 184-187, 1990

A>Title: Primary structure and functional expression of a cyclic nucleotide-activated
A:Reference number: S11517; MUID:90370115; PMID:1697649
A:Accession: S11517
A:Molecule type: mRNA
A:Residues: 1-664 >CHA>
A:Cross-references: GB:X55519; NID:G56791; PIDN:CAA39135.1; PID:G56792
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
C:Keywords: transmembrane protein
F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.0%; Score 804; DB 2; Length 664;
Best Local Similarity 29.6%; Pred. No. 1.1e-41;
Matches 219; Conservative 126; Mismatches 286; Indels 108; Gaps 22;

QY 50 EKS LKTS TPTVTS EEPHTNIQDKLSKNSSGDLTNPDPQNAAEPTGTVPEQK---EMDP 106
DB 4 EKSNGVXSSPANN---HNHPPPSIKANGKDDHRAGSRPQSVAAADDDTSPQLSLAEMDT 60
QY 107 GKEGNSPQNPPAPVINEYADQLH-----NLVGRMQROTALYKKLVGDLSSPE 159
DB 61 PRRGQGQFQIRVLGVIRDWANKNFREBPSPDSFLERFR-----GPE 104
QY 160 ASPQAKPTAVPPVKESDDKTEHYRLLWPKVKOMPLTEYLKRIKLPNSIDSYDRLYL 219
DB 105 LQTVTHQDDKGKDGEGKTKKKFELP-----VLDPAQD-WY 143
QY 220 LWLLLVTL--AYNNCWFPIELRVFPYQADNIHWLADIICDIYLYDMFLTPQRLQF 277
DB 144 RWFVIAAMPVLYNW-CLLAV-ARACFSDLQNVFVWVLVDYFSDTVYIAD-LIIRLTGTF 200
QY 278 VRGDDIIVDSNELKHRYFTSKFOLDVASIIPFDICYLFFGPF-NEMFPAANMLKYTSFFE 336
DB 201 LEQGLLVDPKKLRDNYHTHTQFKLDVASIIPDTLIYFVAGIHSDEVFNRLLHFARPE 260
QY 337 FNHHLESIMDKAYIVRVIRTTGYLEFLIHINACVYVWASNYEGIGTTWVY----DGE-- 390
DB 261 FDRTEHTSPNIFRISNLVLYLVIIHWANACIYVVISKSGFGVDVWVYPNITDPEVG 320
QY 391 --GNEYLCRYNAVATLTIIGGLPPQTLFETVFPOLLNFFSVPFSSLIQMRDVIQAA 448
DB 321 VLAREYIYCLYWSTLTLTIGTTPPVKDEEYLFVDFLIGLVLFATIVNVGWSMISNM 380
QY 449 TANQNYFRACWDDTAYANNYSIPKLQKRVPTWYETWDSQRMLEDSDLLKLTPTVQL 508
DB 381 NATRAEFOAKIDAVKHYNQFRKYSKDMEAKVIKWFIDYLTWNKKTVDREVLKNLFAKURA 440
QY 509 ALAIDVNSIISKVDFLFGKCDTOMYDMLRLKLSVLYLPDGFVCKKGEIGKEMYIIKHGE 568
DB 441 EIAINHLSTLKKVIFQDCEAGILLVELVLRPQVFSFGDYICRKGDIKEMYIIKEGK 500
QY 569 VQVLGGPDGTKVLVTLKAGSVFGEISLLAAG--GNRRATANVAHGFANLLTLDKKTLQ 625
DB 501 LAVV-ADDGVQYALLSAGSCFGEISILNIKSGKMGNNRRNTAIRSLGSDFLCLSKDDLM 559
QY 626 EILVHYPDSERILMKKARVLLKQAKTAB--ATPPRKDALLPFKETPKLFTLLGG 682
DB 560 EAVTEYPDAKVLEERGRSILMKEGILLDENVAASNEVDV-----QEKLEQETNM--D 611
QY 683 TKGASLARLLKLRQAAQKENSEGGEEGEKENEDKQKEN--EDKQKENEDKGENEDK 740
DB 612 TLYTFARLL-----AAYTGAQQLKQRITVLETKQKQNH---EDDYL 651
QY 741 DKGREPEEKPLDRPECTAS 759
DB 652 SDG-----INTPEPTAA 663

RESULT 12
JC6509
rod cyclic nucleotide-gated cation channel protein alpha-chain - dog
C/Species: Canis lupus familiaris (dog)
C/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C/Accession: JC6509

R.Veske, A.: Nilsson, S.E.G.; Gal, A.
Gene 202, 115-119, 1997
A>Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha-subunit
A.Reference number: JG6509; MOID: 98087425; PMID: 9427553
A.Accession: JG6509
A>Status: preliminary
A.Molecule type: DNA
A.Residues: 1-691 <VES>
A.Cross-references: EMBL:X99314; NID: g1489571; PIDN: CAA68186.1; PID: G1489572
A.Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
P.478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match	18.9%;	Score	801.5;	DB	2;	Length	691;
Best Local Similarity	29.2%;	Pred. No.	1.6e-41;				
Matches	220;	Conservative	136;	Mismatches	286;	Indels	112;
Gaps	23;						
QY	21	EQSSRRNEGGHPNSQSQTTAAENKEEKSLLTKSTPVTSEPHNTIOQLSKKNSSG	80	:	:	:	:
Db	24	EKETRMENGARSS-----PSDDGDDDSAMEEES---ENEIPHA--RDSCRNNSQRR	72	:	:	:	:
QY	81	DLTTNPDQNAEPTGTVPQEKMDPGKEGNSPONKPPAAPVINEYADAQLHNVLVKMR	140	:	:	:	:
Db	73	D-----PSQRE-----QYLPGAIALFNVNSSNKEQEPKSK	104	:	:	:	:
QY	141	QRTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKPTHEYHYRLLFWKKMPLTEY	200	:	:	:	:
Db	105	KKKK--EKKSXGSDXNENKXOSEKKKKX-----KEKEKNKEEK-----GDKK--	150	:	:	:	:
QY	201	LKRIKLPSISDYSRDLRYLLMLLVLT--AYNWNCFIPLRLVFFYQYADNIHYWLIADI	258	:	:	:	:
Db	151	KEVAV--IDP-AGNYYNMLFCITLPMYNT--MVIARACFDQLQSDYLEYWIIPDY	204	:	:	:	:
QY	259	ICDITLYDMLFIQPRLOFVRGGDIIVDSNEURKHRYRSTKQOLDVASIIPDICYLFPG	318	:	:	:	:
Db	205	LSDIVLLDM-FVTRTGYLEGLVREBAKLIKYKNLQPKLDFLSVIPDILLYFLKG	263	:	:	:	:
QY	319	FN-PMFRANRMLKYSFPEFNHLESIMDKAYIVRIRTTGVLTLHLINACVYVWASNY	377	:	:	:	:
Db	264	WNYPEIRNLRLIRISRMFEFFORTTRINYPNIFRISNLVMVIVIIHNACVYSISKA	323	:	:	:	:
QY	378	EGIGTRWYV---DGE-----GNEYLRCYVAVRLLITIGGPEPQTUFEIVFQLNFFS	429	:	:	:	:
Db	324	IGFGNDTWYVPDVNDPEFGRLARKVYSLYWSTLTLITIGETPPPPVRDSEYVFWVDFLI	383	:	:	:	:
QY	430	GVYFSSLIQWRDVI GAATANQNTFRACMDOTIAYMNNYSIPKLVOKRAVRYEYTWDS	489	:	:	:	:
Db	384	GVLIPTATIVGNIGSMISNNNAARAEFQARIDAIKQYMHFRNYSKOMKEKVIKWFYDLWN	443	:	:	:	:
QY	490	QRMLESLLKTLPTTVQLALADVNNFSIISKVDLFGCDCTQIMVIMLLRLKSLVLPDG	549	:	:	:	:
Db	444	KKTVDSEKVLKVLPPDKIRAEIILNHLDTLKVRIFADCEAGLLVELVLKLPQVYSPGD	503	:	:	:	:
QY	550	FVCKGGEIKEMYIIKHGEVQVLGGPDGTVLTKAGSVFGEISLLAAG--GNRRTA	606	:	:	:	:
Db	504	YICKKGDIGREMYIIKEGLAVV-ADGITQFVLSDGVSFGEISILINIKSGAGNRRTA	562	:	:	:	:
QY	607	NVVAHFANLLTLDKKTLQEBILVHPDPSRILMKKARVLLKQK-----KTAEATPPRKDL	662	:	:	:	:
Db	563	NIKISYSDLFCLSKDDLMALTEYPDATKMLFEKGQIKMLDKGLLDINIANAGSPDKDL	622	:	:	:	:
QY	663	ALLFPFKETPKFLKTLGGTGKASLARLLKLRQAAQCKENSEGEGEGEKENEDKQKE	722	:	:	:	:
Db	623	EKKVTRMEGSDVLLQT-----RPARIL-----ABEYSMQOK	653	:	:	:	:
QY	723	NEDKQKENEKXKENEKDK-----KGREPEKPLD	752	:	:	:	:
Db	654	IKORIATKVRFLKPIIDTFBSALEGTGDSRPLD	687	:	:	:	:

RESULT 13
S07103
cGMP-gated ion channel protein - bovine
C.Species: Bos primigenius taurus (cattle)

Db 548 VV-AEDGITQFVVLGDSYFGEISILNIKSGNRRRTNIRSIGYSDLCFLSKDOLMEA 606
QY 628 LVHYPDSERILMKKAR-VLLKQK---AKTAEATPPPKDLALLFPKKEETPKLFTLLGGT 683
Db 607 LTEYPEAKKALBEKGQILMKONLIDEEIAKAGADPKD-----EKKVEHLETSLDL 659
QY 684 GKASLARLL-----KLKREQAQKKN 705
Db 660 -QTRFARLLAEYNAQTOMKVQRLSQLES 686
RESULT 15
I50680
alpha subunit of rod photoreceptor CNG-channel - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C;Accession: I50680
R;Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B
Neuron 10, 865-877, 1993
A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
A;Reference number: I50630; MUID:93264082; PMID:7684234
A;Accession: I50680
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-645 <BON>
A;Cross-references: EMBL:X89599; NID:9908852; PIDN:CAA61758.1; PID:9908853
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
F;431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 18.2%; Score 771; DB 2; Length 645;
Best Local Similarity 24.3%; Pred. No. 1.1e-39;
Matches 173; Conservative 104; Mismatches 196; Indels 32; Gaps 12;
QY 217 LYLMLLLVTL--AYNWCNWFILRLVFPYQTDNHIWLIADIICDIIVLYDMLFIQPR 274
Db 116 MYNWLFCITMPVYNNWT--MLTARACFDELQNDYLAWFIVDYVSDVIYIADM-FVTR 172
QY 275 LQVRGGDIIVDSNELKRYTSTKFDLDVASIIPFDICYLFGFN-PMERANRMLKYTS 333
Db 173 TGYLEQGLLVKEQKLEKYSQFKLDFLSIIPDILLYFKLGLNYPELRINRLRVAR 232
QY 334 FFEFNHLESIMDKAVTYRVRTGYLLFILHINACVYVWASNYVEGIGITRWYDGEKN- 392
Db 233 MPEFFQRTETFTNYPNIFRISNLVWYIVIIHWNACVYYSKAIKGFADTVVYNTSHP 292
QY 393 -----EYLCYVAVRTLTITIGLPEPQTLFEIVQLNFPFGVFPVSSLIQOMEDVI 445
Db 293 EFARLTRKYVSLYXWSTLTITIGETPPVRDSEYFFVVDVFLVGLVIFATVGNVSMI 352
QY 446 GAATANQYFRACDDDTIAYNNYSIPKLQKRVRTWYETWDSQRMLESLLKTLPTT 505
Db 353 SNMNAARAEFOAKIDAIKQYHFRVSKDMEKRVIKWFDYLTNKKAVDEREVLKYLDPK 412
QY 506 VQLALADVNPFSIISKVDLFKCDTQMIYDMLRLKSVLYLPDGFVCKKEIGKEMVYIK 565
Db 413 LRABTAINVHLETLKVRIFAIDCEAGLVELVLQVQVSPGDIYCRKGDIGREMYIHK 472
QY 566 HGEVQVLGGPQGTAVTLTKAGSVGEISLAAAGS---GNERTANVAHGAFANLLTLDKK 622
Db 473 EKLAVW-ADGGVQFVVLSDGSGFGEISILNIKSGNRRRTNIRSIGYSDLCFLSKD 531
QY 623 TLQETLVHYPDSERILMKKAR-VLLKQKAKTAEATPPPKDLALLFPKKEETPKLFTLLG 681
Db 532 DLMEALTEYPPDAKAMLEKQILMKQGLLDIEVANLGS-----PKDLEKV--AYME 583
QY 682 GTG----KASLARLLKLKREQAQK 703
Db 584 GSMRLQTKFARL--LAEYDAAQK 606

Search completed: June 21, 2004, 10:07:51
Job time : 25 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:04:22 ; Search time 17 Seconds
(without alignments)
2477.927 Million cell updates/sec

Title: US-09-855-828-1

Perfect score: 4234

Sequence: 1 MFKSLTKVKNKVPIGNEN.....PSAEGGEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1949	46.0	909	1	CNG4_HUMAN
2	1920	45.3	1394	1	CNG4_BOVIN
3	850	20.1	694	1	CNG3_HUMAN
4	831.5	19.6	683	1	CNG1_RAT
5	829	19.6	663	1	CNG2_BOVIN
6	823.5	19.4	684	1	CNG1_MOUSE
7	821.5	19.4	735	1	CNG1_CHICK
8	818.5	19.3	664	1	CNG2_RABIT
9	817	19.3	686	1	CNG1_HUMAN
10	807.5	19.1	682	1	CNG1CTPU
11	804	19.0	664	1	CNG2_RAT
12	801.5	18.9	691	1	CNG1_CANFA
13	797	18.8	690	1	CNG1_BOVIN
14	794	18.8	706	1	CNG3_MOUSE
15	788.5	18.6	631	1	CNG3_MOUSE
16	788.5	18.6	733	1	CNG3_MOUSE
17	777.5	18.4	664	1	CNG3_MOUSE
18	771	18.2	645	1	CNG3_CHICK
19	714	16.9	665	1	CNG3_MOUSE
20	640	15.1	575	1	CNGX_RAT
21	484	11.4	261	1	CNG2_HUMAN
22	427.5	10.1	1175	1	HCN4_RABIT
23	417.5	9.9	1186	1	HCN4_MOUSE
24	414.5	9.8	1198	1	HCN4_RAT
25	413	9.8	1203	1	HCN4_HUMAN
26	412.5	9.7	910	1	HCN1_MOUSE
27	400.5	9.5	889	1	HCN2_HUMAN
28	400.5	9.5	910	1	HCN1_RAT
29	399	9.4	863	1	HCN2_MOUSE
30	397	9.4	774	1	HCN3_HUMAN
31	396	9.4	834	1	HCN2_RAT
32	389.5	9.2	780	1	HCN3_RAT
33	388.5	9.2	779	1	HCN3_MOUSE

ALIGNMENTS

```

RESULT 1
CNG4_HUMAN
ID   CNG4_HUMAN          STANDARD;          PRT;   909 AA.
AC   Q14028; Q14029;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4)
DE   (CNG4) (Cyclic nucleotide-gated cation channel modulatory subunit).
GN   CNGB1 OR CNGC4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS KCNC2A AND KCNC2B).
RC   TISSUE=Retina;
RX   MEDLINE=93226050; PubMed=7682292;
RA   Chen T.Y., Peng Y.-W., Dhallan R.S., Ahamed B., Reed R.R., Yau K.-W.;
RT   "A new subunit of the cyclic nucleotide-gated cation channel in
RT   retinal rods.";
RL   Nature 362:764-767(1993).
CC   -!- SUBUNIT: Heterooligomeric complex with CNG1.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=KCNC2B;
CC   IsoId=Q14028-1; Sequence=Displayed;
CC   Name=KCNC2A;
CC   IsoId=Q14028-2; Sequence=VSP_001110;
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC   (TC 1.A.1.5) family.
CC   -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; L15296; AAA65620.1; -
CC   EMBL; L15297; AAA65619.1; -
CC   XIM; 600724; -
CC   GO; GO:0017071; C:intracellular cyclic nucleotide activated cation channel. ; NAS.
CC   GO; GO:0005222; F:intracellular cAMP activated cation channel. ; NAS.
CC   InterPro; IPR000595; CNMP_binding.
CC   InterPro; IPR005821; Ion_trans.
CC   InterPro; IPR001622; K+channel_pore.
CC   Pfam; PF00027; cnmp_binding; 1.
CC   SMART; SM00100; CNMP; 1.
CC   PROSITE; PS00888; CNMP_BINDING_1; 1.
CC   PROSITE; PS00889; CNMP_BINDING_2; 1.
CC   PROSITE; PS50042; CNMP_BINDING_3; 1.

```

```

34 385.5 9.1 822 1 HCN1_RABIT
35 382.5 9.0 890 1 HCN1_HUMAN
36 365 8.6 1195 1 KCH7_RAT
37 355 8.4 1195 1 KCH7_MOUSE
38 349 8.2 962 1 KCH1_RAT
39 349 8.2 987 1 KCH1_BOVIN
40 341 8.1 1196 1 KCH7_HUMAN
41 337 8.0 988 1 KCH5_RAT
42 336 7.9 989 1 KCH1_MOUSE
43 335 7.9 988 1 KCH5_HUMAN
44 334 7.9 989 1 KCH1_HUMAN
45 327.5 7.7 1162 1 KCH2_MOUSE

```

```

Q9mzsl oryctolagus
Q60741 homo sapien
Q54852 rattus norv
Q9er47 mus musculu
Q63472 rattus norv
O18965 bos taurus
Q9ns40 homo sapien
Q9ep19 rattus norv
Q60603 mus musculu
Q9ncm2 homo sapien
Q95259 homo sapien
O35219 mus musculu

```

KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
 KW Multigene family; Alternative splicing;
 FT DOMAIN 1 314 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 315 333 H1 (POTENTIAL).
 FT DOMAIN 334 347 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 348 366 H2 (POTENTIAL).
 FT DOMAIN 367 391 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 392 411 H3 (POTENTIAL).
 FT DOMAIN 412 448 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 449 471 H4 (POTENTIAL).
 FT DOMAIN 472 515 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 516 535 H5 (POTENTIAL).
 FT DOMAIN 536 619 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 620 640 H6 (POTENTIAL).
 FT DOMAIN 641 909 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 9 29 POLY-GLU.
 FT NP_BIND 628 767 CAMP (BY SIMILARITY).
 FT BINDING 688 688 CAMP (POTENTIAL).
 FT BINDING 700 700 CAMP (POTENTIAL).
 FT VARSPLIC 1 286 Missing (in isoform RCNC2A).
 FT SEQUENCE 909 AA; 102285 MW; DC0E75433686EDDD CRC64;

Query Match 46.0%; Score 1949; DB 1; Length 909;

Best Local Similarity 46.2%; Pred. No. 6.6e-105;
 Matches 403; Conservative 122; Mismatches 238; Indels 110; Gaps 18;

QY 14 IGENNENQSRREBEGHPNQSOQTAAQ--ENKGE---EKLTKTKSTPTVSEEPHTN 68
 DB 67 VGEBAKAEKAEKAEAEVABEAEKPEQDWAETKEPEAEAAASGVPAKQHEVQ 126
 QY 69 IQDK-----LSKNSSGDLTTPDPONAAEPTGTVPQEKMDPGKEGN----- 112
 DB 127 VEDTDADSCPLMAENPPS--TVLPSPSPAKSDTLIVPSSASGTHRKLKLPSEDEABELK 184
 QY 113 --SPONKE-----PAAP-----VINEVADQLNLVKKVRQRTALY 146
 DB 195 ALSPAESPVVAWSPTTPKDTGGDQRAASTASTNSAIND-----RLQELVCLKERTEKV 240
 QY 147 KKLVGDLG----SPEASPTAKTAVPPVKESDDKPT--EHYRLLWFKVKKMPLEUY 200
 DB 241 KEKLIDPDTSDSESPKSPAKAPAPDTPKPAEAPVBEHYCDMLCKFKHRPWKY 300
 QY 201 LKRIKLPSIDYDRLYLMLLVTLAYNNWCFILRLVFPYQATADNIHYHLADIIC 260
 DB 301 ---OFOSIDPLNLMLVTLFFVMAWNNWCLIPVRWAFPYQTDPNHHMLLMDYLC 356
 QY 261 DIIYLDMLFQPRLOFVRGDIIVDSNELRKHRTSTKFLQDVASIPFDICVLPFGFN 320
 DB 357 DLIVFLDITVQTRLOFVRGDIITDKKMNLYLKSRRFKMDLLSLPLDLYLKGVN 416
 QY 321 PMFRANMLKTSPEFNHLESMDKAYIVRTRTGYLLFILHINACVYVWASVEGI 380
 DB 417 PLLRLPCLKTMAYFEFNLSLESLSKAYVVRITRAYLLSLHNSCLYVWASAYQGL 476
 QY 381 GTTRWYDGEVNEVLCYVAVRILITIGLPEPOTLFEIVFOLNFFSGVFFVSSLIQ 440
 DB 477 GSTHWYDGVNSVIRCYPAVKTLITIGLPDKTLFEIVFOLLNFTGVFAFVWMIQ 536
 QY 441 MRDVIGATANTQNTFRACMDTIAVMNYSIPKLVQKRVRTWETWDSQRMLEDSDLLK 500
 DB 537 MRDVVGAATAGCTYRSQMDSTVRYMNFYKIPKSVQNRVKTWETWHSQGMLEDSELMV 596
 QY 501 TLPTTVOLALADYNFSLIKVDLPKCDTOMIYDMLRLKSLVLYLPDGFVCKKGEIGKE 560
 DB 597 QLPKXRLDLADVNYNIVSKVALFQSCDQRMIFDMLKRLRSVYLPNDVYCKKGEIGRE 656
 QY 561 MYIIKHGEVQLGPDGKVLVTLKAGSVFGEISLLAAGGNGRRTANVVAHGPNLLTLD 620
 DB 657 MYIIQAGVQLGPDGKSVLVTLKAGSVFGEISLLAAGGNGRRTANVVAHGPNLFLD 716
 QY 621 KKTIQEILVHPDSEIRIIMKKARVLLKQAKATAPPRKDLALLPPKKEETPKLFTLL 680

Db 717 KKDLNEILVHPESOKLLRKARRMLRGNK-----PKEKSVLILPPRAGTPKLFNAAL 771
 QY 681 GGTGRAS-----LARBLLKREQAOKENSEGEEEEKENEDKQK 728
 Db 772 AMTGRVGGKAGKGLAHLARLKLALALAAKHEEL---VEQAKSODVKGEESGSAAP 828
 QY 729 ENEDKGE-NEDKXGRPEEKFLDRPECTASPIAV-----EEEPHSVVRTVLP 776
 Db 829 DQHTPKERATDPAPRTPPEPP-GSPSPSPASLSGCEGEEGPAPEHSVR----- 882
 QY 777 RGTSGSLIISMAPSAGGEEVLTIVKKAQK 809
 Db 883 -----ICMSPGPPEGEQLSVKMPEREE 906

RESULT 2

CNG4_BOVIN
 ID CNG4_BOVIN STANDARD; PRT; 1394 AA.
 AC Q28181; Q03861; Q28082;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 240 kDa protein of rod photoreceptor CNG-channel (Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel modulatory subunit)).
 DE modulatory subunit)).
 GN CNGB1 OR CNGC4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96009859; PubMed=7546742;
 RA Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A., Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L., Kaupp U.B., Molday R.S.;
 RA "A 240 kDa protein represents the complete beta subunit of the cyclic RT nucleotide-gated channel from rod photoreceptor.";
 RL Neuron 15:627-636 (1995).
 RN [2]
 SEQUENCE OF 454-1394 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96198098; PubMed=8626431;
 RA Biel M., Zong X., Ludwig A., Sautter A., Hofmann F.;
 RA "Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";
 RL J. Biol. Chem. 271:6349-6355 (1996).
 RN [3]
 SEQUENCE OF 1-590 FROM N.A.
 RC TISSUE=Retina;
 RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
 RA Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: Forms functional heterooligomeric channels with CNG3.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=isoform CNG4D is the most frequent isoform (CNG4D:CNG4C:CNG4E = 20:2:1) in testis;
 CC Name=CNG4C;
 CC IsoId=Q28181-1; Sequence=Displayed;
 CC Name=CNG4D;
 CC IsoId=Q28181-2; Sequence=VSP_001109;
 CC Name=CNG4E;
 CC IsoId=Q28181-3; Sequence=VSP_001108;
 CC -!- TISSUE SPECIFICITY: Retina, testis, kidney, heart and brain.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC This SWISS-PROT entry is copy-right. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

RX MEDLINE=95175019; PubMed=7532814;
 RA Distler M., Biel M., Flocke V., Hofmann F.;
 RT "Expression of cyclic nucleotide-gated cation channels in non-sensory
 RL tissues and cells.";
 RN Neuropharmacology 33:1275-1282(1994).
 RP [3]
 RP MEDLINE=98324775; PubMed=9662398;
 RA Kohl S., Marx T., Giddings I., Jaegle H., Jacobson S.G.,
 RA Aplestedt-Sylla E., Zremser E., Sharpe L.T., Wässinger B.;
 RT "Total colour blindness is caused by mutations in the gene encoding the
 RL alpha-subunit of the cone photoreceptor cGMP-gated cation channel.";
 RL Nat. Genet. 19:257-259(1998).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 CC coupled cascade using cGMP as second messenger. This protein can
 CC be activated by cyclic GMP which leads to an opening of the cation
 CC channel and thereby causing a depolarization of cone
 CC photoreceptors.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Prominently expressed in retina.
 CC -!- DISEASE: Defects in CNGA3 are a cause of rod monochromacy (RMCH)
 CC [MIM:216900]; also known as total color blindness or achromatopsia.
 CC RMCH is an autosomal recessively inherited condition.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- DATABASE: NAME=Mutations of the CNGA3 gene;
 CC NOTE=Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/cnga3mut.htm".
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF065314; AAC17440.1; -;
 CC EMBL: S76069; AAD14208.1; -;
 CC PIR: I78560; I78560.
 CC Genew: HGNC:2150; CNGA3.
 CC MIM: 600053; -;
 CC MIM: 216900; -;
 CC GO: GO:0015276; P:ligand-gated ion channel activity; TAS.
 CC GO: GO:0007165; P:signal transduction; TAS.
 CC GO: GO:0006810; P:transport; TAS.
 CC GO: GO:0007601; P:vision; TAS.
 CC InterPro: IPR005821; Ion binding.
 CC InterPro: IPR001622; K-channel_pore.
 CC Pfam: PF00027; CNMP_binding; 1.
 CC Pfam: PF00520; Ion_trans; 1.
 CC SMART: SM00100; CNMP; 1.
 CC PROSITE: PS00888; CNMP_BINDING_1; 1.
 CC PROSITE: PS00889; CNMP_BINDING_2; 1.
 CC PROSITE: PS00890; CNMP_BINDING_3; 1.
 CC Ionic channel; ion transport; CAMP-binding; Transmembrane;
 CC Multigene family; Vision; Disease mutation; Polymorphism.
 CC TRANSMEM 171 192 POTENTIAL.
 CC TRANSMEM 305 325 POTENTIAL.
 CC TRANSMEM 378 397 POTENTIAL.
 CC NP_BIND 482 605 CAMP.
 CC BINDING 549 549 CAMP (POTENTIAL).
 CC BINDING 564 564 CAMP (POTENTIAL).
 CC VARIANT 153 153 T -> M.
 CC /FTid=VAR_010902.
 CC P -> L (in RMCH).
 CC /FTid=VAR_010903.
 CC R -> Q (in RMCH).
 CC /FTid=VAR_010904.
 CC R -> W (in RMCH).
 CC /FTid=VAR_010905.

FT VARIANT 291 291 T -> R (in RMCH).
 FT /FTid=VAR_010906.
 FT VARIANT 410 410 R -> W (in RMCH).
 FT /FTid=VAR_010910.
 FT VARIANT 529 529 V -> M (in RMCH).
 FT /FTid=VAR_010907.
 FT VARIANT 547 547 F -> L (in RMCH).
 FT /FTid=VAR_010908.
 FT VARIANT 557 557 G -> R (in RMCH).
 FT /FTid=VAR_010909.
 SQ SEQUENCE 694 AA; 78838 MW; A500B4EE760D70A0 CRC64;
 Query Match 20.1%; Score 850; DB 1; Length 694;
 Best Local Similarity 30.0%; Pred. No. 9,8e-42;
 Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;
 QY 27 NEEGHPNSQOQTAAQENKGEKSLTKSTPTVSEPHNTIOQKLSKKNSSGDLTNP 86
 DB 5 NTQYSHPS-----RTHLVK-----TSRDNLNRAENGLSRAHSSSETS-- 43
 QY 87 DPQNAAEPTGTVEOKEMDPCKEGNSPKNPPAPVINEVADQHLNVLKRMQRTALY 146
 DB 44 ---SVLQP-GIAMEYRGLADSGQSFTCQ-----GIARLSRLFLRLRWARH 87
 QY 147 KKKLVEGDLSP-----EASQTAKPATVPVVKESDDKPTHEYVRLWFKVKMPL 197
 DB 88 VHHQDQGPDSFPDRFGAEKESVSESNAQANVGSQPADRG-----RSAN-----PL 136
 QY 198 -----TEYLRKIKLPSNI-DSYTDRLYLWLLLVTLAYVWNCWFILRLVFPYQT 246
 DB 137 AKCNTNTNNTEEEKTKKQDAIVDPSSNLYRWLTALPVPFNWLLTLCACFDELQ 196
 QY 247 ADNIHYLIADICDIYLYDMLFIQPRQVVRGDIIVDSNELRKHRYSTKFLQDVAS 306
 DB 197 SEYLMMLVLDYSADVLVLDVL-VRARTGLEQLMVSVDNRLWQHYKTTQPKLDVLS 255
 QY 307 IIPDICYLFGFN-PMFRANRLKYTFPFNHLHSIMDKAYIYVIRTVGLLILH 365
 DB 256 LVPTDLAYLKVGTYNPEVFRNRLKFSLEFFORTTETRTNPNMFRIGNLVILIIH 315
 QY 366 INACVYVWASNYEGIGTRWYVDG-----EGEYLCVYVAVRTLIITIGGLPEPQT 417
 DB 316 WNACIYFALSKEIFGIGTDSWYYPNISPEHGLSRKYISLYWSTLTITIGETPPVKD 375
 QY 418 FEIVFQLNFFSGVFPVSSLLQGMRDVIGATATONQYPRACMDDTIAYMNYSPKLVQK 477
 DB 376 BEYLFVVVDVFLVGLIFATIIVGVGSMISNNVSRAEFOAKIDSIKQYMQFRKTKOLET 435
 QY 478 RVRTWYEVTDQSORMLDESLLKTLPTTVQALALADVNFISIISKVDLFKGDCTOMIDML 537
 DB 436 RVIRWFDVLANKTVDEKVLKSLPDKLKAELINVLHDLTKKVRIFQDCEAGLLVELV 495
 QY 538 LRLKSVLYLPQDGVCKKEIKEMVYIKHGEVQVVGPDGFKVLVTLKAGSVFGEISLLA 597
 DB 496 LKLRPTFSPGDYICKKIDGKEMYYINEGKLAVV-ADGVTQFVWLSGDSYFGEISILN 554
 QY 598 AGG---GNRRTANVAVGFANLLTLDKKTQELIIVHYVDSERILMKKAR-VLLKQK---A 650
 DB 555 IKGSKSGNRRRTANRSIGYSOLFCLSKDLDLMEALTEPEAKKALEEGRQKLDKNLIDE 614
 QY 651 KTAETPPRKDALLLFPKKEETPKLTKTLGGTGKASLARLL-----KLKEQQAQK 702
 DB 615 ELARAGADPKDL-----EEKVEQLGSSL--DTLQTRFARLLAEYNATQMKQKRLSQLE 666
 QY 703 KENSEGEE---EGKENEDKOKENEDKOK 728
 DB 667 SQVKGKDKPLADGGEVPGDATK-TEDKQQ 694
 RESULT 4
 ID_CNG1_RAT
 AC Q62927; Q08659; STANDARD; PRT; 683 AA.

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)
 DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated
 DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
 DE (Rod photoreceptor CGMP-gated channel alpha subunit).
 GN CNGAL OR CNG1 OR CNGC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Barnstable C.J., Wei J.Y.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97287732; PubMed=9142860;
 RA Ding C., Potter E.D., Qiu W., Coon S.L., Levine M.A., Guggino S.E.;
 RT "Cloning and widespread distribution of the rat rod-type cyclic
 RT nucleotide-gated cation channel.";
 RL Am. J. Physiol. 272:C1335-C1344(1997).
 RN [3]
 RN SEQUENCE OF 521-683 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97197878; PubMed=9045728;
 RA Bradley J., Zhang Y., Bakin R., Lester H.A., Ronnett G.V., Zinn K.;
 RT "Functional expression of the heteromeric 'olfactory' cyclic
 RT nucleotide-gated channel in the hippocampus: a potential effector of
 RT synaptic plasticity in brain neurons.";
 RL J. Neurosci. 17:1993-2005(1997).
 CC -1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN
 CC COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN
 CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION
 CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
 CC PHOTORECEPTORS.
 CC -1- SUBUNIT: Homotetramer or higher oligomer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Rod cells in the retina.
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U48803; AAA92110.1; -;
 DR EMBL; U93851; AAC53139.1; -;
 DR EMBL; U76220; AAC17594.1; -;
 DR InterPro; IPR000595; CNGP binding.
 DR InterPro; IPR005821; Ion Trans.
 DR InterPro; IPR001622; K-channel_pore.
 DR Pfam; PF00027; CNGP binding; 1.
 DR Pfam; PF00520; Ion_trans; 1.
 DR SMART; SM00100; CNGP; 1.
 DR PROSITE; PS00888; CNGP BINDING 1; 1.
 DR PROSITE; PS00889; CNGP BINDING 2; 1.
 DR PROSITE; PS00889; CNGP BINDING 3; 1.
 DR PROSITE; PS0042; CNGP BINDING 3; 1.
 KW Ionic channel; Ion transport; CGMP-binding; Transmembrane;
 KW Multigene family; Vision.
 FT DOMAIN 1 155 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 156 176 H1 (POTENTIAL).
 FT DOMAIN 177 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 190 208 H2 (POTENTIAL).
 FT DOMAIN 209 232 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 233 252 H3 (POTENTIAL).
 FT

FT DOMAIN 253 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 313 H4 (POTENTIAL).
 FT DOMAIN 314 365 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 366 385 H5 (POTENTIAL).
 FT DOMAIN 386 469 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 470 490 H6 (POTENTIAL).
 FT DOMAIN 491 683 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 478 600 CGMP (POTENTIAL).
 FT BINDING 537 537 CGMP (POTENTIAL).
 FT BINDING 552 552 CGMP (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 3 4 TN -> KV (IN REF. 2).
 FT CONFLICT 141 141 E -> G (IN REF. 2).
 FT CONFLICT 224 224 E -> K (IN REF. 2).
 SQ SEQUENCE 683 AA; 79228 MW; 62D49F64F8D917C5 CRC64;
 Query Match 19.6%; Score 831.5; DB 1; Length 683;
 Best Local Similarity 30.5%; Pred. No. 1.1e-40;
 Matches 212; Conservative 133; Mismatches 263; Indels 87; Gaps 20;
 QY 71 DKLSKSSGDLTTNPPQNAEPTGVPEQKMDPG-----KSPNSPQNKPPAAP 122
 DB 24 EKIRRMENGACSSFSNDN-----GSLSESENEDSLFRNSYRRRGPSQREHYLPTGM 78
 QY 123 V---INEYADAQLHNLVKRMQROTALYKKLVGEGDLSPEASQPTAKPTAVPPVKESDDK 179
 DB 79 ALENNVNSSNKDQDPKPKKKKKK---EKKSKADKKESKDDPKKKKKKKKKKKKK 134
 QY 180 PTEHYRLWFKVKKMPLETVLKRILKLENSDSYDRLYLMLLLVTL--AYNNCWFIP 237
 DB 135 PRE-----KK---EEKKEVVV---DP-SGNMYNNLFCITLPVNNWT--MI 175
 QY 238 LRLVFPYQADNIHYLIADIICDIYLYDMLFQPRQLQFVRGGDIIVDSNELRKHRTS 297
 DB 176 ARACEDELQSDYLEWLIIFYDVSVVYLDWM-FVTRTGYLEQGLVVDKELKIEKKAN 234
 QY 298 TKFQLDVASIIPFCYCLFPGFN-PMFRANRMLKYSFFEFNHLESIMDKAYIVRVT 356
 DB 235 LQFKLDVLSVPTDLLYKFGWNYPEIRNLRLLSRMFEFFQRTETNTYENFRISNL 294
 QY 357 TGYLLFIHLINACVYVYASNVYEGITTRWY---DGE---GNEYLRCYVAVRVLTI 408
 DB 295 VMYIVIIHWACVYISKISKAIGFNDTWVYDNDPFGRLARKYVYSLWSTLTITI 354
 QY 409 GGLPEFQTLFELVQLNFFSGVVFSSLIQOMRDVIGAAATANQNYFRACDDTIAYNN 468
 DB 355 GETPPVLDSEYFVVVDFLIGVLIFATIVGNIGSMISNMNAARAEFQSRVDAIKQYNNF 414
 QY 469 YSIPKLVKVRVRYEYTWDSQMLDESLLKTLPTTVQLALADVNFSTISKVDLPKGC 528
 DB 415 RNVSXDMKRVIKWFDYLTWNTKKTVDREVRVLPDKURAEIANNVHLDTLKKVRFAD 474
 QY 529 DTQMIYDMLLRKLSVLYLPFGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTVLTKAGS 588
 DB 475 EAGLLVELVVKLOPVYSPGDYICKKGDIGREMYIIKSGKLAVV-ADDGITQFVVLSDGS 533
 QY 589 VFEISLLAAGG---GNERTANVAHGAFANLLTDKKTLQELLVHYPSERILMKKARVL 645
 DB 534 YFEISILNKGSKAGNRRTANIKSIGYSDFLCUSDLDLMEALTYPDAKTMLSEKGRQI 593
 QY 646 LKQKA---KTAETPPRKDALALLFPKPEETPKLEKTLGGTGKASLARLL-----K 693
 DB 594 LMKDGLLDINIANLGSDPKLEKTVMEGSDVLLQT-----RFAILAEYSEMQOK 645
 QY 694 LKREQAQKK-----ENSEGGEERKEN 716
 DB 646 LKQRLTKVEKFLKPLIETEFSALEPFGGESEPTES 680
 RESULT 5
 CNG2_BOVIN STANDARD; PRT; 663 AA.
 ID_CNG2_BOVIN
 AC_Q03041;

[illegible]

DR	InterPro: IPR005821; Ion trans.	
DR	InterPro: IPR001622; K+channel_pore.	
DR	Pfam: PF00027; CNMP binding; 1.	
DR	Pfam: PF00520; ion trans; 1.	
DR	SMART: SM00100; CNMP; 1.	
DR	PROSITE: PS00888; CNMP BINDING 1; 1.	
DR	PROSITE: PS00889; CNMP BINDING 2; 1.	
DR	PROSITE: PS00892; CNMP BINDING 3; 1.	
DR	PROSITE: PS00942; CNMP BINDING 3; 1.	
KW	Ion channel; Ion transport; CAMP-binding; Transmembrane;	
KW	Multigene family; Olfaction.	
FT	DOMAIN 1 140	
FT	TRANSMEM 141 160	
FT	DOMAIN 161 173	
FT	TRANSMEM 174 192	
FT	DOMAIN 193 216	
FT	TRANSMEM 217 237	
FT	DOMAIN 237 274	
FT	TRANSMEM 275 297	
FT	DOMAIN 298 349	
FT	TRANSMEM 350 369	
FT	DOMAIN 370 453	
FT	TRANSMEM 454 474	
FT	DOMAIN 475 664	
FT	NP BIND 462 584	
FT	BINDING 521 521	
FT	BINDING 536 536	
FT	CARBOHYD 379 379	
SQ	SEQUENCE 664 AA; 5E9170D0B322B3E9 CRC64;	
	19.3%; Score 818.5; DB 1; Length 664;	
	Best Local Similarity 29.7%; Pred. No. 6.1e-40;	
	Matches 218; Conservative 127; Mismatches 289; Indels 99; Gaps 20;	
QY	50 EKSLKTKSTVTSEEPHTNIQDKLSKNSGDTTNPDPQNAAPGTVPQK--EMDPG 107	
DB	3 EKNGVKSSPANN--HNNVPTATIKANGKDESTRSRQSAADDDTSSELQRLAEMDAP 59	
QY	108 KEGNSPQNKPPAAPVINEVA-----DAQLNLRMRQRTALYKKLVGEGDLSSPA 160	
DB	60 QQRGGFRIRVLVGVIRQWNRNFRFEARPDPSFLERF-----GPEL 103	
QY	161 SPQTAKTAVPPVKESDDKTEHYRLWFKVKKMPLETKRLPNSIDSYTDRLYLL 220	
DB	104 QTVTQGGDKGDKGDKGDKKKKFLF-----VLDPAGD-WYR 142	
QY	221 WLLIVLT--AYNNCWFPIRLVFPYQTADNIHYLIADIICDIYLYDMLFTQPKLQV 278	
DB	143 WLFVIAMPVLYNW-CLLV-ARACFSDLRQGVFLVWLVDFSDVVIAD-LFIRLRGTGL 199	
QY	279 RGGDIIVDSNELRKHHTSTKFLQDVASIIIPDICYLFFGF-NMPFRANRMLKYSFFEF 337	
DB	200 EQGLLVKDPKLRDNYIHTLQFKLDVASIITPDLIYFAVGIIHNPFLRNFLLHFARMPEF 259	
QY	338 NHLESIMDKAYIVRVITRTGYLLFILHINACVYVWASNYEGIGTTRWVY----DGE--- 390	
DB	260 FDRTEITSFNPFRISNLVLIYLIHWNACIYAIKSGISGVDVWVYFNITDPEYGY 319	
QY	391 -GNEYLCRYWAKVTLITIGLPPQPLFEIVPOLNFFSGVFFVSSLLIQMDRVDIGAT 449	
DB	320 LAREYIYCLVWSTLTATIGTTPPVKDBEYLFVIFDPLGVLFAIVNGVSMISNMN 379	
QY	450 ANQNYFRACDDTAYMNNYSIPKLQKRVETWYETWDSORMLDESDLLKTLPTTVOLA 509	
DB	380 ATRAEFAQIDAVGHYHQFRKVSKEAKVWKWFDYLTWTKVTVDREVLKNLPKRLAE 439	
QY	510 LAIDVNFYSIKVDFKFGCDTQMTYDMLLRKSLVLYLPQDFVCKKGIGKEMIIKGEV 569	
DB	440 IAINVHLSTLKKVIRFQDCEAGLLVELVLRQPVQFSGDYICRKGIGKEMIIKGEKL 499	
QY	570 QVLGPDGTQVLVTLKAGSVFGEISLLAAG--GNERTANVVAHGFANLLTLDKKTLOE 626	
DB	500 AVV-ADGGVTQYALLSAGCFGEISILNKGSKVGNRTANIRSLGYSDFLCISKDLM 558	

QY	627 ILVHPDSEIRILMKARVLLKQAKTAE---ATPPRKDALALLPPPKETPKLFTLLGGT 683	
DB	559 AVTEYPPDAKKVLEERGIEILMKSGLLDENEVAASMEVDVQEKLKQLETNNTLYTRFG-- 616	
QY	684 GKASLARLLKLKREQAQKENSEGGEKEKEDKCKEN--EDKOKENEDKCKENEDKD 741	
DB	617 -----RL-----ABYGAQQLKQRIITVLEVKQKQNT-----DDYLS 651	
QY	742 KGREPEEKPLDRP 754	
DB	652 GMSPEFAAAEQP 664	

RESULT 9

CNG1_HUMAN	STANDARD;	PRT;	686 AA.
ID	CNG1_HUMAN		
AC	P29973; Q16279; Q16485;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	cGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)		
DE	(Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated		
DE	channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)		
DE	(Rod photoreceptor cGMP-gated channel alpha subunit).		
GN	CNG1 OR CNG1 OR CNG3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]_SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Retina;		
RX	MEDLINE=92210603; PubMed=1372302;		
RA	Pittler S.J., Lee A.K., Altherer M.R., Howard T.A., Seldin M.F.,		
RA	Hurwitz R.L., Wasmuth J.J., Baehr W.;		
RT	"Primary structure and chromosomal localization of human and mouse		
RT	rod photoreceptor cGMP-gated cation channel.";		
RL	J. Biol. Chem. 267:6257-6262(1992).		
RN	[2]_SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Retina;		
RX	MEDLINE=92356211; PubMed=1379636;		
RA	Dhallan R.S., Macke J.P., Eddy R.L., Shows T.B., Reed R.R.,		
RA	Yau K.-W., Nathans J.;		
RT	"Human rod photoreceptor cGMP-gated channel; amino acid sequence,		
RT	gene structure, and functional expression.";		
RL	J. Neurosci. 12:3248-3256(1992).		
RN	[3]_SEQUENCE OF 313-573 FROM N.A.		
RP	SEQUENCE OF 313-573 FROM N.A.		
RX	MEDLINE=95175019; PubMed=7532814;		
RA	Disler M., Biel M., Flockerzi V., Hofmann F.;		
RT	"Expression of cyclic nucleotide-gated cation channels in non-sensory		
RT	tissues and cells.";		
RL	Neuropharmacology 33:1275-1282(1994).		
RN	[4]_VARIANT ARRPPH-316, AND VARIANTS GLN-28 AND ASN-114.		
RP	VARIANT ARRPPH-316, AND VARIANTS GLN-28 AND ASN-114.		
RX	MEDLINE=96036047; PubMed=7479749;		
RA	Driva T.P., Finn J.T., Peng Y.-W., McGee T.L., Berson E.L., Yau K.-W.;		
RT	"Mutations in the gene encoding the alpha subunit of the rod		
RT	cGMP-gated channel in autosomal recessive retinitis pigmentosa.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 92:10177-10181(1995).		
CC	-I- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN		
CC	COUPLED CASCADE USING CIMP AS SECOND MESSENGER. THIS PROTEIN CAN		
CC	BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION		
CC	CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD		
CC	PHOTORECEPTORS.		
CC	-I- SUBUNIT: Homotetramer or higher oligomer. Forms heterooligomeric		
CC	complex with CNG4.		
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-I- TISSUE SPECIFICITY: Rod cells in the retina.		
CC	-I- DISEASE: Defects in CNGA1 are a cause of autosomal recessive		
CC	retinitis pigmentosa (ARRP) [MIM:123825]. ARRPP is a disease that		
CC	leads to degeneration of retinal photoreceptor cells.		

equally well by both cAMP and cGMP.
 CC -!- TISSUE SPECIFICITY: Olfactory neurons.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M83111; -; NOT_ANNOTATED_CDS.
 DR PIR; JH0560; JH0560.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K+channel pore.
 DR InterPro; IPR001201; PAP_25A_core.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; Ion_trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; 1.
 DR PROSITE; PS00889; cNMP_BINDING_2; 1.
 DR PROSITE; PS50042; cNMP_BINDING_3; 1.
 DR Olfaction; Ion transport; Ionic channel; cAMP-binding; cGMP-binding;
 KW Transmembrane. 1
 KW DOMAIN 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 H1 (POTENTIAL).
 FT DOMAIN 158 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 159 H2 (POTENTIAL).
 FT DOMAIN 170 H2 (POTENTIAL).
 FT TRANSMEM 190 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 191 H3 (POTENTIAL).
 FT TRANSMEM 219 H3 (POTENTIAL).
 FT DOMAIN 240 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 H4 (POTENTIAL).
 FT DOMAIN 294 H4 (POTENTIAL).
 FT TRANSMEM 311 H5 (POTENTIAL).
 FT DOMAIN 332 H5 (POTENTIAL).
 FT TRANSMEM 333 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 344 H6 (POTENTIAL).
 FT TRANSMEM 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 455 CAMP (BY SIMILARITY).
 FT NP_BIND 455 CAMP (POTENTIAL).
 FT BINDING 514 CAMP (POTENTIAL).
 FT BINDING 529 CAMP (POTENTIAL).
 SQ SEQUENCE 682 AA; 78020 MW; 2C78597DC2C74F75 CRC64;
 Query Match 19.1%; Score 807.5; DB 1; Length 682;
 Best Local Similarity 29.0%; Pred. No. 2.7e-39;
 Matches 192; Conservative 137; Mismatches 256; Indels 77; Gaps 17;
 QY 119 PAAPVINEYAD-----AQLNLVKKMRORTALYKKVLEGLSSPEA-----SPQAKPT 168
 Db 55 PSAEMLEAFTQRRPLARLVNLVLSIREWA---HKSLVETE-QRPDSFLERFRGQAAANDQ 110
 QY 169 AVPPVKESDDKPTHEYHYELLWFKVKMPLTEYLKRIKLPNSIDSYTRLYLLWLLVTLA 228
 Db 111 SAAPA-----DAPKTF-----KEREGFVVSQSDIYYWLFIALA 148
 QY 229 --YNNWCWIFLRLVFPYQADNHYWLIADIIDIIYLYDMLFIQPLQVFRGDIIVD 286
 Db 149 SLYNW--IWLVARACFDQLQDENPFLWGLVLCVIVILDTCLRLRTGYLEQGLVKD 205
 QY 287 SNELKHYRTSTKFDVASIIPDCIVLFGFPMFANRMLKXYSFEFENHLESIMD 346
 Db 206 LAKLRDNYRTQLKDFLSLPTLLEFFVYGVYQPLFNRLFRSMFEFDDTEFTN 265
 QY 347 KAYIVRVIRTTGYLLFILHINACVYMASNVEGIGTTTWNVYDGGNE----YLRCYWAV 402
 Db 266 YPNAFCINLILYILVIHWNACIYVJASKALGLSSDTWVYSGQNTLSFCYVCYFWST 325
 QY 403 RFLITIGLPEPQTLFEIVFQQLNFFSGVFFPSSILGQVRDVIGATANQYFACWDDT 462
 Db 326 LTLTITIGEMPPPVKDEEYVYVVDLVLGVLIFATIVGVNGSMIANNATRAEFQTRIDAI 385

QY 463 IAYMNNYSIKPLVOKRVRTWVEYTWDSQRMDESDLLKTLPTTVQLALAIQVNFYSISKV 522
 Db 386 KHYMHFKVNTLETRVWKFDYLTWNTKVTDEQVLKNLPDKLRABIAINVLHDLTKKV 445
 QY 523 DLFKGGDTQMIYDMLLKLKSVLYLPDGFVCKKGEIKHEMYIIKHGEVQVLGGPDGTVLV 582
 Db 446 RIFQDCEAGLLVELVLRPQVYSPGYICRKDGIGKEMVYIIEGQLAVV-ADGVQTQPA 504
 QY 593 TLKAGSVFGEISLLAAGG---GNRRTANVVAHGPNALLTLDKKTLOEILVHYPSERILM 639
 Db 505 LTTAGGCGEISILNIQSKMGKRNRTANIRSIGVSDLFCLSKDLMKMEVAEYPAQKVL 564
 QY 640 KKARVLLKQAKTAAATP-----PRKDLALLPPPKETPKLFTILG---GT 683
 Db 565 ERGREILRKQGLLDESVAAGGLGVIDTEEKVERLDASL-----DILQTRFARDLGEFTST 619
 QY 684 GKASLARLLKLKBEQA-----AQKENSEGGEEG---KENEDKQKEDKQKEDKKE 736
 Db 620 QRRLKQRITALERQLCHTGLGLLSDNEAGEHAGVPTHADIHAQETHRTSAETNSE 679
 QY 737 NE 738
 Db 680 EE 681
 RESULT 11
 CNG2 RAT STANDARD; PRT; 664 AA.
 ID CNG2 RAT Q00195;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
 DE cation channel 2) (CNG channel 2) (CNG2) (CNC1).
 GN CNGA2 OR CNCG2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory sensory neuron;
 RX MEDLINE=90370115; PubMed=1697649;
 RA Phallan R.S., Yau K.-W., Schrader K.A., Reed R.R.;
 RT "Primary structure and functional expression of a cyclic nucleotide-
 RT activated channel from olfactory neurons.";
 RL Nature 347:184-187(1990).
 CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-
 CC protein coupled cascade using cAMP as second messenger. The
 CC olfactory channel can be shown to be activated by cyclic
 CC nucleotides which leads to a depolarization of olfactory sensory
 CC neurons.
 CC -!- SUBUNIT: Heterooligomer of CNCA1 and CNCA2 subunits.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Olfactory neurons.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X55519; CAA39135.1; -;
 DR PIR; S11517; S11517.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR005821; Ion_trans.

DR InterPro: IPR001622; K+channel_pore.
 DR Pfam: PF00027; CNMP binding; 1.
 DR Pfam: PF00520; ion Trans; 1.
 DR SMART: SM00100; CNMP; 1.
 DR PROSITE: PS00888; CNMP_BINDING_1; 1.
 DR PROSITE: PS00889; CNMP_BINDING_2; 1.
 DR PROSITE: PS0042; CNMP_BINDING_3; 1.
 KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 142 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 143 162
 FT DOMAIN 163 175 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 176 194
 FT DOMAIN 195 218 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 219 238
 FT DOMAIN 239 276 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 277 299
 FT DOMAIN 300 351 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 352 371
 FT DOMAIN 372 455 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 456 476
 FT DOMAIN 477 664 CYTOPLASMIC (POTENTIAL).
 FT NP BIND 464 586 CAMP (BY SIMILARITY).
 FT BINDING 523 523 CAMP (POTENTIAL).
 FT BINDING 538 538 CAMP (POTENTIAL).
 FT CARBOHYD 381 381 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 212 212 K -> R.
 SQ SEQUENCE 664 AA; 76176 MW; 720806950EC27F3C CRC64;

Query Match 19.0%; Score 804; DB 1; Length 664;
 Best Local Similarity 29.6%; Pred. No. 4.2e-39;
 Matches 219; Conservative 126; Mismatches 286; Indels 108; Gaps 22;

QY 50 EKSLLTKSTPTVSEPHNTIQQKLSKNSGDLTTPDPQNAEPTGTVPQEK---BMDP 106
 DB 4 EKSNGVKSSPANN---HNHPPPSIKANGKDDHAGSRPQSVAAADDTSPQLQLAEMDT 60
 QY 107 GKEGNSQNPAPVINEYADQLH-----NLVKRMQRTALYKKLVEGDJSSPE 159
 DB 61 PRGRGGQFQIRLVGVIRWDWANKFNFRPEEPRPSFLERFR-----GPE 104
 QY 160 ASPQAKTAVPPVKESDDKTEHYKLLWFKVKKMPLTEYLKRIKLPNSIDSYDRLYL 219
 DB 105 LQTVTHQDDKGGKGGKTKKKKFLF-----VLDPAGD-WYY 143
 QY 220 LWLLLVTL--AYNNCWPIPLRVFPYQTDNIHWLIADIICDIYLYDMLFIQRLQF 277
 DB 144 RWLFVIAMPVLVYN-CLLV-ARACFSDLQRYNFVWLVLDVFSVTYVIAI-LIIRLTGF 200
 QY 278 VRGDIIVDSNELKHYRTSKFOLDVASIIPDICVLFYGF-NPMFRANMLKYTSFFE 336
 DB 201 LEQGLLVKDPKLDNIHTIQFQKLDVASIIPDIIYFVAGIHSPEVFRNLLHFARMEF 260
 QY 337 FNHLESIMDKAYIRVIRITGYLLFLILHINACVYVWASNYEGITGRWYV-----DGE-- 390
 DB 261 FFDRTETRTSPNIFRISNLVLYLIIHWNACIYVYSKISGFGVDWYVNPITDPEYG 320
 QY 391 --GNEYLRCYVWARTLITIGLPEPQTLPEIYVOLLNFFSGVFFVSSLLGQMRDVIGAA 448
 DB 321 YLAREYICLYWSLTLTITIGETPPVPVKDEYLFVIFDFLIGLFIATIVNGVMSNM 380
 QY 449 TANQNYFRACDDTIIATMNNYSIPKLVQKVRVWYETWDSQRMLESLLKTLPTVOL 508
 DB 381 NATRAEFOAKIDAVKHYVQKFKVSKDMEAKVKKFVLYLWTKNTVDERVILKPLAKLA 440
 QY 509 ALAIDVNFISIISKVDLFGKCDTQIMVIMLRLKSLVLYPGDFVCKGEGTKGMYIIKHGE 568
 DB 441 EIAINVHLSTLKKVRFQDCAGLLVELVILKRPQVFSFGDYICRKGDIKGEMYIIKEGK 500
 QY 569 VOVLGGPDGTVLTVLTKAGSVFGEISILLAAAG---GNRRATANVVAHGFANLLTLDKTLQ 625
 DB 501 LAVV-ADGGVTOYALLSAGSCFGEISILNKGSGMGNRRATANIRSLGYSDLCFLSKDDLM 559

QY 626 EILVHPDPSERILMKKARVLLKOKAKTAE---ATPPKDLALLFPKERTPKLFTLLGG 682
 DB 560 EAVTEYPAKVKLEERGLIMKEGLLDENVAASMEVDV-----QEKLEQLTNN--D 611
 QY 683 TGRASLARILKLRQAQAQKENSEGEGEKENEDKOKEN--EDQKQKENEKQKENEK 740
 DB 612 TLYTRFARLL-----AETGAQKKQKQRTIVLETQKQKQNH-----EDDYL 651
 QY 741 DKGREPEEKPLDRPECTAS 759
 DB 652 SDG-----INTPEPTAA 663

RESULT 12
 CNG1_CANFA STANDARD; PRT; 691 AA.
 ID CNG1_CANFA
 AC Q28279;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CNGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)
 DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated
 DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
 DE (Rod photoreceptor CNGMP-gated channel alpha subunit).
 DE CNG1 OR CNG1 OR CNGC.
 GN Canis familiaris (Dog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Beagle X Briard;
 RA Veske A.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97415722; PubMed=9268598;
 RA Zhang Q., Pearce-Kelling S., Acland G.M., Aguirre G.D., Ray K.;
 RT "Canine rod photoreceptor CNGMP-gated channel protein alpha-subunit:
 RT studies on the expression of the gene and characterization of the
 RT cDNA."
 RL Exp. Eye Res. 65:301-309(1997).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 CC coupled cascade using cGMP as second messenger. This protein can
 CC be activated by cGMP which leads to an opening of the cation
 CC channel and thereby causing a depolarization of rod
 CC photoreceptors.
 CC -!- SUBUNIT: Homotrimer or higher oligomer.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X99314; CAB68186.1; -;
 CC EMBL: U83905; AB61707.1; -;
 CC PIR: JC6509; JC6509.
 CC InterPro: IPR00595; CNMP binding.
 CC InterPro: IPR005821; Ion Trans.
 CC InterPro: IPR001622; K-channel_pore.
 CC Pfam: PF00027; CNMP binding; 1.
 CC Pfam: PF00520; ion Trans; 1.
 CC SMART: SM00100; CNMP; 1.
 CC PROSITE: PS00888; CNMP_BINDING_1; 1.
 CC PROSITE: PS00889; CNMP_BINDING_2; 1.
 CC PROSITE: PS50042; CNMP_BINDING_3; 1.

KW	Ionic channel; Ion transport; cGMP-binding; Transmembrane;	
KW	Multi-gene family; Vision.	
FT	DOMAIN 1 163	
FT	TRANSSEM 164 184	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 185 197	H1 (POTENTIAL).
FT	TRANSSEM 198 216	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 217 240	H2 (POTENTIAL).
FT	TRANSSEM 241 260	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 261 298	H3 (POTENTIAL).
FT	TRANSSEM 299 321	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 322 373	H4 (POTENTIAL).
FT	TRANSSEM 374 393	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 394 477	H5 (POTENTIAL).
FT	TRANSSEM 478 498	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 499 691	H6 (POTENTIAL).
FT	NP BIND 486 608	CGMP (POTENTIAL).
FT	BINDING 545 545	CGMP (POTENTIAL).
FT	BINDING 560 560	CGMP (POTENTIAL).
FT	CARBOHYD 424 424	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE 691 AA; 80251 MW; 0775CAA42F065275 CRC64;	
	Query Match 18.9%; Score 801.5; DB 1; Length 691;	
	Best Local Similarity 29.2%; Pred. No. 6.1e-39;	
	Matches 220; Conservative 136; Mismatches 286; Indels 112; Gaps 23;	
QY	21 EQSRRNEGSHSNQSQQTAEENKGBEKSLLTKSTPTVSEPHNINQDKLSKNSG 80	
DB	24 EKEIRMEGARS-----FSDDDGDDASAFEE-----ENETPHA--RDCRNSQRR 72	
QY	81 DLTTNPQNAEPTGTVPRQKEMDPCGEGNSPQNKPPAAPVINEYADLAQLHNVKRM 140	
DB	73 D-----PSORE-----QYLPGAIALFNVNSSNKEQEPKEK 104	
QY	141 QRTALYKKLVGDLSPSPQAKTAVPPVKESDDKTEHYRLLWFKVKKMPLTEY 200	
DB	105 KKKK--EKSKSGDKNENKDKSEKKKKE-----KEKEKKKEK-----GKOKK---EE 150	
QY	201 LKRIKLSNDSYDRLYLWLLVLT--AYNNCWPIPLRLVFPVQTADNIHYLIADI 258	
DB	151 KKEVWV---IDP-AGNYYNWLFCITLPVMYNT--NVIAACFDELQSDYLEVWIFDY 204	
QY	259 ICDIYIYDMLFIQPRQIVRGDIIIVDSNELKHTSTKPKQLDVAIIPFDICVLF 318	
DB	205 LSDIYVLLDM-FVTRTGYLEQGLVREARLKEKYKSNLQKLDLFLSVIPTDLLFKLG 263	
QY	319 FN-PMFANRMLKVTSPFEFNHLESIMDKAYIVRVIRTCYLLFIHINACVYVWASNY 377	
DB	264 WNYEILNLLRLSRMFEPFQRTETRNPNFRISNLVWYVILHWNACVYFSLSKA 323	
QY	378 EGICITRWVY-----DGE-----GNEYLRCYVAVETLITIGLPEPOTLFEIVQLNFFS 429	
DB	324 IGFNGDTWVVDNDPFGRLARKYVSLYVSTLTLTIGETPPPPVDSYVVFVVDVFLI 383	
QY	430 GVVFSSLIQMDVIGANATQNYFRACDDTITAYNNYSIPKLKVRVTVVETWDS 499	
DB	384 GVLFIATVIGNIGMNMNARAEFQARIDAIKQYHFRNVSMDKEKVIKFDYLVWNT 443	
QY	490 QRMDESLLKTLPTVQLALAIQVNFSTISKVDLFKGCQDTQMTIYDMLLRKSLVYLP 549	
DB	444 KKTVDKELVKVLPDLKLBABTAINVHLDLTKKVRIFADCEAGLLVVLVLPQVVSFGD 503	
QY	550 FVCKKGETGKEMIIKHEVOVLGPDGTVKLVTLKAGSVFGEISILAAG---GNRTA 606	
DB	504 YICKKGDIGREMYIIKEGLAVV-ADDGITOFVVLSDGSVFGESILNIRKSGKAGNRTA 562	
QY	607 NVVAGFANLTLDKTLQELTIVHPDSEITLMKKARVLLKQKA-----KTAEPAPPKDL 662	
DB	563 NIKSIGVSDLCFLSKDDLMEALTEYTPDAKTMLEKQKILMDGLDINIANAGSDPKDL 622	
QY	663 ALLFPPEETPKLFTLIGTGKASLARLLKLRQAAQKENSEGEEGKEKNEKQKE 722	
DB	623 EEKVTREMGSDLLQT-----RFAIL-----AEYESMQKK 653	

QY	723 NEDQKQKEDKQKEDKD-----KGRPEEKPLD 752	
DB	654 LKQRLTKVERFLKPIIDTFSALEGTGDESRLD 687	
	RESULT 13	
QY	CNG1_BOVIN	STANDARD; PRT; 690 AA.
ID	CNG1_BOVIN	
AC	Q00194;	
DT	01-APR-1993 (Rel. 25, Created)	
DT	01-APR-1993 (Rel. 25, Last sequence update)	
DT	15-MAR-2004 (Rel. 43, Last annotation update)	
DE	CGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)	
DE	(Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)	
DE	(Rod photoreceptor cGMP-gated channel alpha subunit).	
GN	CNGA1 OR CNCG1 OR CNCG.	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC	Bovidae; Bovinae; Bos.	
OX	NCBI_TaxID=9913;	
RN	[1]	
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RC	TISSUE=Retinal rod cell;	
RX	MEDLINE=90098076; PubMed=2481236;	
RA	Kaup U.B., Nildome T., Tanabe T., Terada S., Boenigk W., Miyata T.,	
RA	Stuehmer W., Cook N.J., Kangawa K., Matsuo H., Hirose T.,	
RA	Numa S.;	
RT	"Primary structure and functional expression from complementary DNA	
RT	of the rod photoreceptor cyclic GMP-gated channel.";	
RL	Nature 342:762-766(1989).	
RN	[2]	
RP	3D-STRUCTURE MODELING OF 485-610.	
RX	MEDLINE=92256398; PubMed=1316156;	
RA	Kumar V.D., Weber I.T.;	
RT	"Molecular model of the cyclic GMP-binding domain of the cyclic GMP-	
RT	gated ion channel.";	
RL	Biochemistry 31:4643-4649(1992).	
RN	[3]	
RP	TOPOLOGY.	
RX	MEDLINE=95365381; PubMed=7543681;	
RA	Henn D.K., Baumann A., Kaupp U.B.;	
RT	"Probing the transmembrane topology of cyclic nucleotide-gated ion	
RT	channels with a gene fusion approach.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7425-7429(1995).	
RN	[4]	
RP	TOPOLOGY.	
RX	MEDLINE=92112723; PubMed=1370452;	
RA	Wolffart P., Haase W., Molday R.S., Cook N.J.;	
RT	"Antibodies against synthetic peptides used to determine the topology	
RT	and site of glycosylation of the cGMP-gated channel from bovine rod	
RT	photoreceptors.";	
RL	J. Biol. Chem. 267:644-648(1992).	
CC	!- FUNCTION: Visual signal transduction is mediated by a G-protein	
CC	coupled cascade using cGMP as second messenger. This protein can	
CC	be activated by cGMP which leads to an opening of the cation	
CC	channel and thereby causing a depolarization of rod	
CC	photoreceptors.	
CC	!- SUBUNIT: Homotetramer or higher oligomer.	
CC	!- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	!- TISSUE SPECIFICITY: Rod cells in the retina.	
CC	!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel	
CC	(TC 1.A.1.5) family.	
CC	!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	

CC DR EMBL; X51604; CAA35947.1; -
 DR PIR; S07103; S07103.
 DR InterPro; IPR00595; cNMP_binding.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; Ion_trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; 1.
 DR PROSITE; PS00889; cNMP_BINDING_2; 1.
 DR PROSITE; PS00442; cNMP_BINDING_3; 1.
 KW Ionic channel; Ion transport; cGMP-binding; Transmembrane;
 Multigene family; Vision.
 FT DOMAIN 1 162
 FT TRANSMEM 163 183
 FT H1 (PROBABLE).
 FT DOMAIN 184 196
 FT EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 197 215
 FT H2 (PROBABLE).
 FT DOMAIN 216 239
 FT CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 240 259
 FT H3 (PROBABLE).
 FT DOMAIN 260 297
 FT EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 298 320
 FT H4 (PROBABLE).
 FT DOMAIN 321 372
 FT CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 373 392
 FT H5 (PROBABLE).
 FT DOMAIN 393 476
 FT EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 477 497
 FT H6 (PROBABLE).
 FT DOMAIN 498 690
 FT CYTOPLASMIC (PROBABLE).
 FT NP_BIND 485 607
 FT BINDING 544 544
 FT CGMP (POTENTIAL).
 FT BINDING 559 559
 FT CGMP (POTENTIAL).
 FT CARBOHYD 423 423
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 690 AA; 79602 MW; A0LCFB6567424455 CRC64;
 Query Match 18.8%; Score 797; DB 1; Length 690;
 Best Local Similarity 29.3%; Pred. No. 1.1e-38;
 Matches 212; Conservative 129; Mismatches 282; Indels 100; Gaps 19;
 QY 8 VNKVPIGNNENQSSRRNEEGSHPSNQSQTAAQENKGEKSLKTPVTSBPHT 67
 DB 13 VNIPNVGPDVEKETRMENAGCSFGSDDDDSAMFEES-----ETENPHA 59
 QY 68 NIQDL-SKKSSGDLITNPQNAAPTGTVPQKEMDPCKGPNPQKPAAPVINE 126
 DB 60 --RDSFRSNTGSGQ-----PSQRE-----QYLPGAIALFNV 89
 QY 127 YADAQLHNLVGRMORTALYKXKLVGDLSPASPOKAPTAVPPVKESDDKTEHYR 186
 DB 90 NNSNKEQEPKEXKXKXK--EKSKPDDKNENKXDPKXKXK-----KDKXKXKES-- 140
 QY 187 LLWFVKKQKPLTEYLKRIKLPNSIDSVYDRLLYLWLLVTL--AYNWNCFPIPLRLVFPY 244
 DB 141 ----KGDKKXEEKVVDPSGNTYNN-----WLCITLPVWYNT--MILARACFDE 199
 QY 245 QTANIHWLADIICDIYLYMLFTQIPQFVRGGDIIVDSNELKXRTSTKPOLDV 304
 DB 190 LQSDYLEWLAFLDVLSDVVYLLDN--FVTRTRGYLEQGLKVEERKLDKXKSTFQFQLDV 248
 QY 305 ASIIPEDICYLFFGN--PMFRANRLKVTSPFENHLESIMDKAYIYRVIRTTGYLLFI 363
 DB 249 LSVIPTDLYLKGNVPEIRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 308
 QY 364 LHINACVYVWASNYEGITTRWYDGBN-----EYLCRYVAVRTLTITIGLPEPQ 415
 DB 309 IHNACVYVFSKAIQFGNDTWYVDVNDPDPFGRLARKYVSLYSLWSTLTITIGETPPV 368
 QY 416 TLEIIVFOLLNFFSGVFVESLIGMDVIGAAQANQYERACDDTIAVMYNSIPKLV 475
 DB 369 RDSYFFVADFLGLVIFATIGNISMISNNMAARAEQARLDAIKQWHPFRNVSMD 428
 QY 476 QKRVTYEYTDWSQRLMDSLLKLTPTTVQLALADVNFSISKVDLFGCDTQMIYD 535
 DB 429 EKRVIKFDYLTWNTKKTVDREVLKLPDLKRLABIAINVHLDTLKKVRIEADCEAGLVE 488

QY 536 MLRLKSLVLYLPQDFVCKKGEIGKEMYYIIKHGEVQVLGGPDGKTVLVTIKAGSVFEISL 595
 DB 489 LVLKLPQVYSPCDYICKGDIQREMYIIKEGLAVV-ADDGITQFVVLSDGSYGEISL 547
 QY 596 LAAGG---GNRTANVAVGFANLTLTKKTYQETILVHYDSEIRILMKARVLLKOKA-- 650
 DB 548 LNIKSGKAGNRRTANIKSIGYSDLFCLSKDDLMLEALTEYFDKGMLEKQKQILMKDGLL 607
 QY 651 --KTAEATPRKDLALLPPPKETPKLTKTLGGTGKASLARLL-----KLKREQAA 700
 DB 608 DINIAGSDPKDLBEKVTRMESSVLLLOT-----RFAILAEYSMQOKLQRLTK 659
 QY 701 QKX 703
 DB 660 VEK 662
 RESULT 14
 CNG3_BOVIN
 ID CNG3_BOVIN STANDARD; PRT; 706 AA.
 AC Q29441;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
 DE (CNG-3) (CNG3) (Cyclic nucleotide-gated channel alpha 3) (Cone
 DE photoreceptor cGMP-gated channel alpha subunit).
 GN CNGA3 OR CNCG3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94211295; PubMed=7512693;
 RA Weyand I., Godde M., Frings S., Weiner J., Mueller F., Altenhofen W.,
 RA Hatt H., Kaupp U.B.;
 RT "Cloning and functional expression of a cyclic-nucleotide-gated
 RT channel from mammalian sperm."
 RL Nature 368:859-863 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=94224768; PubMed=8170936;
 RA Biel M., Zong X., Distler M., Bosse E., Klugbauer N., Murakami M.,
 RA Flockerzi V., Hofmann F.;
 RT "Another member of the cyclic nucleotide-gated channel family,
 RT expressed in testis, kidney, and heart."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3505-3509 (1994).
 CC -!- FUNCTION: Could be responsible for cGMP-induced calcium entry in
 CC cells other than sensory cells. Might be involved in chemotaxis of
 CC sperm.
 CC -!- SUBUNIT: Forms functional heterooligomeric channels with CNG4 in
 CC vitro.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Testis, kidney, retinal cone and heart.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; X89600; CAA61759.1; -
 CC EMBL; X76485; CAA54023.1; -
 CC PIR; A55251; A55251.

DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; ion trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING_1; 1.
DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR PROSITE; PS00890; cNMP BINDING_3; 1.
DR PROSITE; PS00442; cNMP BINDING_3; 1.
KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
KW Multigene family; Vision.
FT TRANSMEM 186 206 POTENTIAL.
FT TRANSMEM 322 342 POTENTIAL.
FT TRANSMEM 398 418 POTENTIAL.
FT NP_BIND 501 624 CAMP.
FT BINDING 568 588 CAMP (POTENTIAL).
FT BINDING 583 583 CAMP (POTENTIAL).
SQ SEQUENCE 706 AA; 81132 MW; P4990DCD29B56239 CRC64;

Query Match 18.8%; Score 794; DB 1; Length 706;
Best Local Similarity 29.7%; Pred. No. 1.7e-38;
Matches 204; Conservative 141; Mismatches 263; Indels 80; Gaps 19;

QY 69 IQDKLSKNSGDLTNPDPQNAEPGTGVPKEMDPGKEP-----111
DB 28 IENGLSRTHLPCEETSSELQEGIAMETRGIAESRQSFTSQGPTRLSLRIISLRAWSARH 87
QY 112 -NSPQKPPAPVINEVADQLNLVKEQRTALYKKLVGDLSSPE-----ASQ 163
DB 88 LHQEDQPDG--FLERFRGALQEVSR-----ESHVQNVQSQQPPDRGRSAWPL 136
QY 164 TAKPTAVPPVKESDDKPTETHYRLLWFKVKMPLTEYLK--IKLPNSIDSYDRIYLLW 221
DB 137 ARNNTNCNNSKDDKAKKE-----KXKEEKENPKKEKKDSVMDPSSNMYHW 190
QY 222 L--LLVTLANWNCWTFPLRVPYQYADNIHNLWLTADIICDIYLYDMLFIQPRLOFVR 279
DB 191 LTVIAVPVFNW--CLLV-CRACFDELQSEHLMLWLDYSADILYGDMDL--VEARTGFLE 247
QY 280 GGDIIVDSNELRKHRTSTRFQDLVASIIPDFICYLPFGFN--PMFRANRLMKYTSFEFN 338
DB 248 QGLWMDASRLKHYIQTQLHKLVDLSLPTDLAYFKLGNVYELFRLNLLKLARLEFF 307
QY 339 HHLESIMKAYIVRVIRTTGYLFIHLINACVYVWASNYEGITTRWYDGN-----392
DB 308 DRTETRTNYNPRFIGNLVLYLIIHWNACIYFAISKFTGFGTDSWVYVNSNPNYGR 367
QY 393 --EYLRCYVAVRTLIITIGLPPQTLFEIVFOLLNPFSGVVFSSLIQMRDVIQAATA 450
DB 368 SRKIYSLWSTLTITIGTPPPVDEEYLFVVIDFLGVLFATVGVNVMGNMNA 427
QY 451 NQNYFRACMDDTIAYMNNYIPKLQKRVRTWYEYTWDSQRMDESDLLKLTPTTTLAL 510
DB 428 SRAEFQAKIDSIKQYMQFRKVTQDLTRVIRWFDYLVANKKTVDKXEVLSKLPDLKAEI 487
QY 511 AIDVNFSLISKVDLFCQDQMIYDMLRLKSVLYLPDGVCKGKGTGKEMVLIKHGEVQ 570
DB 488 AINVHDLTKRVRIFQCEAGLVVLKURPAVSPGDIYCKKGDIGREMYIIKKGKLA 547
QY 571 VLGGPDGTVLVLTKAGSFGVGEISLLAAGG---GNRTANVAVHGFANLLTLDKTLOEI 627
DB 548 VV-AEDGITQVVLGDSYFGVGEISILNKGSKGNRRRTANIRSGYSDLPCLSKDDLMEA 606
QY 628 LVHVPDSERILMKAR-VLLKQK---AKTAEATPPKDLALLPPKREETKFLKTLGGT 683
DB 607 LTEYPEAKALEEGRQILMKDNLIDEELAKAGADPKDI-----BEKVEHLETSLDSL 659
QY 684 GKASLARLL-----KLKREQAAQKEN 705
DB 660 -QTRFARLLAEYNATQMKVQRLSQLES 686

CNG3_MOUSE
ID CNG3_MOUSE STANDARD; PRT; 631 AA.
AC Q9JUZ8; Q9WV01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE (CNG-3) (CNG3) (Cyclic nucleotide gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN CNGA3 OR CNGB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=20273944; PubMed=10813773;
RA Hirano A.A., Hack I., Waessle H., Duvoisin R.M.;
RT "Cloning and immunocytochemical localization of a cyclic nucleotide-
RT gated channel alpha-subunit to all cone photoreceptors in the mouse
RT retina";
RL J. Comp. Neurol. 421:80-94 (2000).
RN [2]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=99307448; PubMed=10377453;
RA Biel M., Seeliger M., Pfeifer A., Kohler K., Gerstner A., Ludwig A.,
RA Jaisle G., Fauser S., Zrenner E., Hofmann F.;
RT "Selective loss of cone function in mice lacking the cyclic
RT nucleotide-gated channel CNG3";
RL Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557 (1999).
CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
CC coupled cascade using cGMP as second messenger. This protein can
CC be activated by cyclic GMP which leads to an opening of the cation
CC channel and thereby causing a depolarization of cone
CC photoreceptors.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Prominently expressed in retina.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ243933; CAB89685.1; -;
CC EMBL; AJ238239; CAB42891.1; -;
CC EMBL; AJ238240; CAB42891.1; JOINED.
CC EMBL; AJ238241; CAB42891.1; JOINED.
CC MGD; MGI:1341818; Cng3.
CC GO; GO:0005221; F:intracellular cyclic nucleotide activated c...; IPI.
CC InterPro; IPR000595; cNMP_binding.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR001622; K-channel_pore.
CC Pfam; PF00027; cNMP_binding; 1.
CC Pfam; PF00520; ion_trans; 1.
CC SMART; SM00100; cNMP; 1.
CC PROSITE; PS00888; cNMP BINDING_1; 1.
CC PROSITE; PS00889; cNMP BINDING_2; 1.
CC PROSITE; PS00442; cNMP BINDING_3; 1.
CC Ionic channel; Ion transport; CAMP-binding; Transmembrane;
KW Multigene family; Vision.
FT TRANSMEM 112 133 POTENTIAL.
FT TRANSMEM 244 264 POTENTIAL.
FT TRANSMEM 320 340 POTENTIAL.
FT NP_BIND 423 546 CAMP.
FT BINDING 490 490 CAMP (POTENTIAL).

```

FT BINDING      505      505      CAMP (POTENTIAL) .
FT CONFLICT    110      110      C -> Y (IN REF. 2).
FT CONFLICT    157      157      L -> V (IN REF. 2).
SQ SEQUENCE    631 AA; 72641 MW; 4FA8CD3B9AA3FE6C CRC64;

Query Match
Best Local Similarity 33.1%; Score 788.5; DB 1; Length 631;
Matches 177; Conservative 110; Mismatches 212; Indels 35; Gaps 13;

QY 214 TDRLLVLLVLLVTLA--YNNMCWFPLRLVFPYQTADNIHYHLIADIICDIIILYDMLFI 271
Db 105 SSNIYCRWLTAIALPVTNNW-CLLV-CRACDELOQSEHLTLMLVDYSADVLVYLDML-V 161

QY 272 QPRLOFVRGGDIIIVDSNELRKHRTSTKFDLDVASIIPFDICYLFFGFN-PMFANRMLK 330
Db 162 RARTGFLSQGLMVRDTKRLWGHYTKTLHFKLDILSLIPTDLAYLKLGVNYPELAFRNLKX 221

QY 331 YTSPEFNHLESINDKAYIYRVIRTTCYLFILHINACVYWNASNYEGIGTTRWYVDGE 390
Db 222 FSRUFEFDRTRTETNPNVFRIGNLVLYTLIIHWNACIYFAISKFIGFGTDSWVYPNT 281

QY 391 -----GNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFOLLNFPFSGVFVSSLIQMR 442
Db 282 SKPEYARLSRKXIYSLYWSLTJLTIGETPPVKDEEYLFVVIDFLVGILIFATIVGVG 341

QY 443 DVIGATANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSQRLMDSDLKTL 502
Db 342 SMISNMNAPRVFOAKIDSVRQYMQFRKVTXDLFTRVIRWFDYLVANRKTVDKEVLKNL 401

QY 503 PTTQLALAIIDVNTSIIISKVLEKGCDFQMIYDMLRLKSVLPLPGDFVCKGKEIGREMY 562
Db 402 PDKLAEIINVHLDLTKKVRIFQDCAGLLEUULVLRPTVPSPGDIICKGDI GREMY 461

QY 563 IIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAG--GNRRTANVVAHGFANLLTL 619
Db 462 IIKGKLAVV-ADGVTQFVVLSDGSYFGEISILNKGSKSGNRRTANIRSIGVSDLFCL 520

QY 620 DKTLQELVHYPPSERILMKAR-VLLKQAKTAEATPPRKOLALLFPPEETPKLFKT 678
Db 521 SKDDLMEALTEYPAKALEEKQIILMKONLIDEDLVAARVDTR----DVEEKVEYLES 576

QY 679 LLGGTGKASLARLL-----CLKRQA---AOKENSEGGBEGKENEDKOK 721
Db 577 SL-DILQTRFARLLAEYSASQWKLKQRLTRLESQWNERCCGFSFDPDRENSSEDASK 629

```

Search completed: June 21, 2004, 10:06:12
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:04:22 ; Search time 23 Seconds
(without alignments)
1815.887 Million cell updates/sec

Title: US-09-855-828-1

Perfect score: 4234
Sequence: 1 MFKSLTKVNVKPIGNNEN.....PSAEGGBEVLTVIEYKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	818.5	19.3	690	4	US-09-275-252A-19
2	484	11.4	261	4	US-09-275-252A-18
3	412.5	9.7	910	4	US-08-997-685A-2
4	382.5	9.0	749	4	US-08-997-685A-10
5	382	9.0	528	4	US-08-997-685A-4
6	370	8.7	597	4	US-08-997-685A-12
7	368	8.7	506	4	US-08-997-685A-6
8	360.5	8.5	960	4	US-09-694-777A-21
9	349	8.2	987	4	US-09-694-777A-22
10	347.5	8.2	962	4	US-09-694-777A-24
11	345.5	8.2	962	4	US-09-614-480-9
12	345.5	8.2	962	4	US-08-694-777A-3
13	344	8.1	170	4	US-08-358-383C-27
14	337	8.0	988	4	US-10-162-012-12
15	336	7.9	988	4	US-09-694-777A-23
16	335	7.9	988	4	US-09-614-480-2
17	335	7.9	988	4	US-10-162-012-5
18	334	7.9	988	4	US-09-358-383C-22
19	334	7.9	989	4	US-09-694-777A-4
20	317.5	7.5	1159	2	US-08-956-242-13
21	317.5	7.5	1159	3	US-08-351-215-13
22	317.5	7.5	1159	3	US-09-236-012-2
23	317.5	7.5	1159	3	US-09-236-012-4
24	317.5	7.5	1159	4	US-09-358-383C-10
25	317.5	7.5	1159	4	US-09-275-252A-12
26	302.5	7.1	857	4	US-09-275-252A-11
27	294	6.9	888	2	US-08-956-242-4

28	294	6.9	888	3	US-09-351-215-4	Sequence 4, Appli
29	291.5	6.9	1107	4	US-09-358-383C-16	Sequence 16, Appl
30	282.5	6.7	597	4	US-09-275-252A-7	Sequence 7, Appl
31	268.5	6.3	1102	4	US-09-358-383C-36	Sequence 36, Appl
32	266	6.3	126	4	US-08-997-685A-58	Sequence 58, Appl
33	265.5	6.3	129	4	US-08-997-685A-46	Sequence 46, Appl
34	258	6.1	1083	4	US-09-358-383C-2	Sequence 2, Appli
35	257	6.1	1082	4	US-09-336-643A-20	Sequence 20, Appl
36	257	6.1	1083	4	US-09-600-776-2	Sequence 1, Appli
37	257	6.1	1083	4	US-09-343-494-1	Sequence 2, Appli
38	253.5	6.0	1017	4	US-09-600-776-6	Sequence 6, Appli
39	253	6.0	1284	4	US-09-343-494-9	Sequence 9, Appli
40	253	6.0	1284	4	US-09-358-383C-11	Sequence 11, Appl
41	247.5	5.8	126	4	US-08-997-685A-57	Sequence 57, Appl
42	215	5.1	189	4	US-09-358-383C-25	Sequence 25, Appl
43	174	4.1	542	4	US-09-358-383C-5	Sequence 5, Appli
44	167.5	4.0	131	4	US-08-997-685A-45	Sequence 45, Appl
45	165.5	3.9	119	4	US-08-997-685A-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1									
US-09-275-252A-19									
; Sequence 19, Application US/09275252A									
; Patent No. 6641997									
; GENERAL INFORMATION:									
; APPLICANT: The Rockefeller University									
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With									
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation									
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof									
; FILE REFERENCE: 018512-002901US									
; CURRENT APPLICATION NUMBER: US/09/275,252A									
; CURRENT FILING DATE: 1999-03-24									
; PRIOR APPLICATION NUMBER: US 09/045,529									
; PRIOR FILING DATE: 1998-03-20									
; PRIOR APPLICATION NUMBER: US 09/054,347									
; PRIOR FILING DATE: 1998-04-02									
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307									
; PRIOR FILING DATE: 1999-03-22									
; NUMBER OF SEQ ID NOS: 42									
; SOFTWARE: Patent in Ver. 2.1									
; SEQ ID NO 19									
; LENGTH: 690									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-275-252A-19									
Query Match									
Best Local Similarity 30.0%; Pred. No. 5e-64;									
Matches 221; Conservative 128; Mismatches 262; Indels 125; Gaps 22;									
QY	5	LTKNVKKVPIGNNENFSSRRNEEGSHPS	---	NOSQQTAAOEKNGBE	-----	KSL	53		
Db	17	VTMNVIVP	----	DIEKEIRRMENGACSSFS	SEDDSDSAYTSESENNENPHARGSPYSKSL	71			
QY	54	MTKSTPTVTSSEPHNIQDKLSKNSSGDLTNPDPQNAAEPTGTVPPEKEMDFGKEGPN	113						
Db	72	R-KGSPSQREQYLPFGAIAIFNVANSS	-----	NKD	----	QEPPEKKKKKKKKKKSDKNE	121		
QY	114	PONKPPRAAPVINEYADALHNLVKRMFORALYKVKLVGDLSSPEASPTAKTAPVPV	173						
Db	122	NNNTP	-----	KKKKKKKEKKK	-----	E	141		
QY	174	KESDDKPTHEHYRLWLPKVKMPLTEYLKRIKLPNSIDSYTDRLYLWLLVLT	231						
Db	142	EKSXDKKEHH	-----	KKEVVV	-----	IDP-SGNTYNNWLPFCITLPVWYV	180		
QY	232	NCWFILRLVFPYQADNIHVMFIADITCDIIVLYDMLFIQPLQFVRGGDIIVDSNEAR	291						
Db	181	T-MVIARACPELQSDYLEFWLILDIIVSDIVILIDM-FVTRTGTGLEQLVKEELKI	237						

QY 292 KHYRSTKQDVASIIPDICYLFFGFN-PMFRANRMLKYTSFFPFNFHLESIMDKAYI 350
Db 238 NKYSKQLKFLDVLISLIPDLYFLKGNYPPIRLNRLLSBMEFFQRTETRTNYPNI 297
QY 351 YVIRITGGLFILHINACVYTWASNYEGIGTRWY-----DGE-----GNEYLRCCYVAV 402
Db 298 FRISNLVYVYIIHWNACVYSISKAIGFGNDTWVYPIINDPEFGRILARKYVYSLYWST 357
QY 403 RLITIGGLPEPQTLFEIYFOLLNFFSGVVFSSLIGOMRDVIGATATONVFRACMDT 462
Db 358 LTLTIGETPPVRDSEYVFWVDLGLVLPATVGNIGSMISNNARAEFQARDAI 417
QY 463 IAYMNYISPKLVQKRVTRTWBYTWSORMLDESLLKTLPTTVQALALDYNFISIISKV 522
Db 418 KQMHFRNVSKDMKRVIKWFDYLTNKTVDKEVLKYLDPKLRARAEIATNVLHDLTKV 477
QY 523 DLFKGCDDTQMIYDMLRLKSLVLYLPQDFVCKGGEIGKEMYYIKHGEVQVGLGPGDKVLY 582
Db 478 RIFADCEAGLLVELVKLPQVYSGDYCKRGDIGREMYIKHGEKLAUV-ADGVTQFV 536
QY 583 TLKAGSVFGEISLLAAGG---GNRETANVVAHGFANLLTLDKTLQELVHYPPSERILM 639
Db 537 VLSGSGTTFGEISILNIKSGKAGNRRTANIKSIGVSDFLCFLSKDDLMEALTEYDPAKTMLE 596
QY 640 KQARVLLKQKA-----KTAERTPPKDLALLFPKPEETPKPLKTLGGTGKASLARLL--- 692
Db 597 EKGQILMKDGLLDLNIANAGSDPKOLEBEKVTREMGVDDLQOT-----RFAILAEY 648
QY 693 -----KLXREQAAQK 703
Db 649 ESMQOKLQRLTKVEK 664
RESULT 2
US-09-275-252A-18
; Sequence 18, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-18

Query Match 11.4%; Score 484; DB 4; Length 261;
Best Local Similarity 37.2%; Pred. No. 7e-35;
Matches 97; Conservative 58; Mismatches 94; Indels 12; Gaps 4;
QY 370 VYTWASNYEGIGTRWY-----DGE-----GNEYLRCCYVAVRLLITIGGLPEPQTLFEIV 421
Db 1 IYVAISKIGFVDVTPYPIITPEVGYLAREIYCLYWSLTLTITIGTPPPVDEEVL 60
QY 422 FOLLNFFSGVVFSSLIGOMRDVIGATATONVFRACMDTIIAYMNYISPKLVQKRVTR 481
Db 61 FVIFDELIGLIFATIVGNVGSIMNNATRAEFOAKIDAVKHVMQFRKVSKGMEAKVIR 120

QY 482 WYEVWDSORMLDESLLKTLPTTVQALALDYNFISIISKVDLFGCDDTQMIYDMLRLK 541
Db 121 WPYLWTKKTVDERILKNLPAKLRARAEIATNVLHDLTKKVRIFHDCEAGLLVELVKLR 180
QY 542 SVLYLPQDFVCKGGEIGKEMYYIKHGEVQVGLGPGDKVLYTLKAGSVFGEISLLAAGG- 600
Db 181 PQVSPGDYICRKGDIKEMYYIKHGEKLAUV-ADGVTQVALLSAGSCFGEISILNIKGS 239
QY 601 --GNRETANVVAHGFANLLTL 619
Db 240 KMGNRRTANIRSLGYSDDLFLCL 260
RESULT 3
US-08-997-685A-2
; Sequence 2, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 910
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (130)..(148)
; OTHER INFORMATION: S1
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (164)..(185)
; OTHER INFORMATION: S2
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (208)..(229)
; OTHER INFORMATION: S3
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (243)..(271)
; OTHER INFORMATION: S4
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (291)..(313)
; OTHER INFORMATION: S5
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (332)..(358)
; OTHER INFORMATION: P
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (367)..(387)
; OTHER INFORMATION: S6
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (472)..(602)
; OTHER INFORMATION: CNB
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC53518
; DATABASE ENTRY DATE: 1997-12-27
; RELEVANT RESIDUES: (1)..(910)
US-08-997-685A-2

Query Match 9.7%; Score 412.5; DB 4; Length 910;
Best Local Similarity 20.2%; Pred. No. 1.1e-27;
Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;
QY 210 IDSYTD-RLVLLWLLLVTLAYNWCNCFIPLRLPPYQTDNIHVLADIICDIYLYDM 268

Db 124 IHPYSDFRFY--WDLIMLMMVGNLVIIPVGITF--FTEQTTTFWIFNVASDTVELLDL 179
QY 269 LFIQRLQFVRG-----GDIIVDSNELRKHYRTSTKFQDVASIIPDFICYL----- 315
Db 180 I-----MNFRTGTVNEDESSEIILDPKVIKMYLKSWM-FVVDFFISSIPVDYIFLIVEKGM 233
QY 316 -----FFGFENFRANRMLKYSFPEFNHLESIMDKAY-----IYRVITTYG 359
Db 234 SEVYKTARALIRVFTKILSLRLRLRLIRYTHOWEEIFHMTYDLASAVRIFNLGM 293
QY 360 LFIILHINACVY-----WASNYEGITTRWYVDGEGNEYLRCYVAVRTLIT 407
Db 294 MLLCHWDGCLQFLVLLQDPDPDCWVSLNE-----MVNDSMGKQVSYALFKAMSHMLC 347
QY 408 IG-GLPEPQTLFEIVFOLLNFPFSGVFFVSSLIQOMRDVIGAAATANQNYFRACMDDTIAYM 466
Db 348 IGYGAQAPVMSDMLWITMLSNIVGATCYAMFVGHATALIQSLDSSRRQYOEKQYQVEQYM 407
QY 467 NNYISPKLVQKRVRTWYETWDSQMLDESLLKTLPTTVQLALADVNFS-----IISKVD 523
Db 408 SFHKLPAQMRQKIHDIYEHRYQG-KIFDEENILSELNDPLREBI--VNFNCRKLVATMP 463
QY 524 LFKGCDTQMIYDMLRLKSVLYLPDGFVCKKGEGIKEMYLKKEGVQVLGGPGDKTVLVT 583
Db 464 LFANADPNFVTAMLSKURFEVQFGDYIIRREGAVGKMYFIQHGAVGI-----TKSKE 518
QY 584 LKA--GSVFGESISLAAGGNRRRTANVAHGFANLLTLDKKTQLQELIVHYPDSE 637
Db 519 MKLTDGSGVFGICLLTKG--RRTASVRADTYCRLYSLSVDNENFVLEVPMMRRAFETV 575
QY 637 -----ILMKK-----ARVLLKQKAK----- 551
Db 576 AIDRLDRGKNSILLQKQKDLNTGVNNOENILKQIVKHDRMVQALIPPINYPQMTA 635
QY 652 ---TAEATPPRKDL-----ALLFP-----P 668
Db 636 LNCITSTTTPSRMTQSPVYATSLSHSNLHSPSPSTQTPQSAILSPCSYTTAVCSP 695
QY 669 KEETPKLFTLLGGTKASLARILKLKREQAQ---KKENSEGEBEGEKENEKQENED 725
Db 696 PIQSPLATRTTHYASPTASQSLSLKQPPQQLPQSQVQQTQTTQOQOQOQOQOQOQOQ 755
QY 726 KQKNEDEKGENEDKGRPEEKPLDRPCTASPIAVEBEPHSVRRTVLPRTQSL- 784
Db 756 QOQ 755
QY 785 -----IISMAFSAGGEBVLTI 801
Db 816 HEVSTLIS-RHPHTVGESLASI 836

RESULT 4
US-08-997-685A-10
; Sequence 10, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 749
; TYPE: PRT
; ORGANISM: human
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC39759
; DATABASE ENTRY DATE: 1998-05-29
; RELEVANT RESIDUES: (1)..(749)

US-08-997-685A-10
Query Match 9.0%; Score 382.5; DB 4; Length 749;
Best Local Similarity 23.8%; Pred. No. 4e-25;
Matches 119; Conservative 99; Mismatches 196; Indels 87; Gaps 18;
QY 210 IDSYTD-RLYLWLLLLVTLAYNWCWFILRLRFPVQTDADNIHYWLIADICDIILYLYDM 268
Db 14 IHPYSDFRFY--WDLIMLMMVGNLVIIPVGITF--FTEQTTTFWIFNVASDTVELLDL 69
QY 269 LFIQRLQFVRG-----GDIIVDSNELRKHYRTSTKFQDVASIIPDFICYL----- 315
Db 70 I-----MNFRTGTVNEDESSEIILDPKVIKMYLKSWM-FVVDFFISSIPVDYIFLIVEKGM 123
QY 316 -----FFGFENFRANRMLKYSFPEFNHLESIMDKAY-----IYRVITTYG 359
Db 124 SEVYKTARALIRVFTKILSLRLRLRLIRYTHOWEEIFHMTYDLASAVRIFNLGM 183
QY 360 LFIILHINACVY-----WASNYEGITTRWYVDGEGNEYLRCYVAVRTLIT 407
Db 184 MLLCHWDGCLQFLVLLQDPDPDCWVSLNE-----MVNDSMGKQVSYALFKAMSHMLC 237
QY 408 IG-GLPEPQTLFEIVFOLLNFPFSGVFFVSSLIQOMRDVIGAAATANQNYFRACMDDTIAYM 466
Db 238 IGYGAQAPVMSDMLWITMLSNIVGATCYAMFVGHATALIQSLDSSRRQYOEKQYQVEQYM 297
QY 467 NNYISPKLVQKRVRTWYETWDSQMLDESLLKTLPTTVQLALADVNFS-----IISKVD 523
Db 298 SFHKLPAQMRQKIHDIYEHRYQG-KIFDEENILSELNDPLREBI--VNFNCRKLVATMP 353
QY 524 LFKGCDTQMIYDMLRLKSVLYLPDGFVCKKGEGIKEMYLKKEGVQVLGGPGDKTVLVT 583
Db 354 LFANADPNFVTAMLSKURFEVQFGDYIIRREGAVGKMYFIQHGAVGI-----TKSKE 408
QY 584 LKA--GSVFGESISLAAGGNRRRTANVAHGFANLLTLDKKTQLQELIVHYPDSE 637
Db 409 MKLTDGSGVFGICLLTKG--RRTASVRADTYCRLYSLSVDNENFVLEVPMMRRAFETV 465
QY 638 -----LMKKARVLLKQKAK 651
Db 466 AIDRLDRGKNSILLQKQKDLNTGVNNOENILKQIVKHDRMVQALIPPINYPQMTA 635

RESULT 5
US-08-997-685A-4
; Sequence 4, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 528
; TYPE: PRT
; ORGANISM: mouse;
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC40125
; DATABASE ENTRY DATE: 1998-05-29
; RELEVANT RESIDUES: (1)..(504)
US-08-997-685A-4
Query Match 9.0%; Score 382; DB 4; Length 528;
Best Local Similarity 24.4%; Pred. No. 2.6e-25;
Matches 129; Conservative 95; Mismatches 213; Indels 92; Gaps 20;
QY 202 KRIKLPNS--IDSYTD-RLYLWLLLLVTLAYNWCWFILRLRFPVQTDADNIHYWLI 256
Db 18 ERVKSAGAWIHPYSDFRFY--WDLTMLLPMVGNLIIIPVGITFFKDETTAP---WIVF 71

Db 301 IYGRQAVGMSDVWLTWLSMIVCATCYAMFIGHATALIOSLSSRRQYQEKQVQW 360
QY 467 NNYISPKLVQKRVRTWYBTWDSQMLDESLLKTLPTTQALADVNFS----LISKVD 523
Db 361 SPKLPPTQRIHDIYEHRYQG-KMFEDESILGELSEPLREET---INFNCRLVASMP 416
QY 524 LFKGCDTQMIYDMLRLKSVLYLPQDFVCKKGEIGKEMVLIKHGEVOVLGGPDGTVLVT 583
Db 417 LFANADPNFVSMTLKLPFEVQGDYIIRGTICKMYTIOGVSVL--TKGKE-TR 473
QY 584 LKAGSVGEISLLAAGGNRRRTANVVAHFANLTL 619
Db 474 LADGSYFGEICLLTRG---RETASVRADTYCRLYSL 506
RESULT 8
US-09-694-777A-21
; Sequence 21, Application US/09694777A
; Patent No. 6638736
; GENERAL INFORMATION:
; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL
; APPLICANT: STUHRER, WALTER
; APPLICANT: BECKH, SYNNOVE
; APPLICANT: BRUGEMANN, ANDREA
; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO
; APPLICANT: PEREZ, ARACELI SANCHEZ
; APPLICANT: WESELOH, RUDIGER
; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: MPG-8
; CURRENT APPLICATION NUMBER: US/09/694,777A
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: PCT/EP99/02695
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EP 98 10 7268.9
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 21
; TYPE: PRT
; LENGTH: 960
; ORGANISM: Bovine sp.
US-09-694-777A-21

Query Match 8.5%; Score 360.5; DB 4; Length 960;
Best Local Similarity 20.2%; Pred. No. 5.3e-23;
Matches 129; Conservative 120; Mismatches 257; Indels 133; Gaps 22;
QY 221 WLLVTLAYNWCNFIPLRLVFPY-----QTADNHYWLIADIICDIILYDML-----F 270
Db 222 WIIILITFT-----AIIVPYNVSFKTRQNNVAVLWVDSIVDVIFLVDIVLNFHTTF 273
QY 271 IOPRLQFVRGGDIIVDSNELRKHRTSTKFOLDVASIIPEDICYLF-----FGNPMFRAN 326
Db 274 VGP-----AGEVISDPKLIEMNY-LKTFWVIDLLSCLPYDVINAFENVDEGISLSS 326
QY 327 RMLKVTSP-----FBNHLESIMDKATYIRVTGTYLLFILHINACVYTWASNYE----- 378
Db 327 KVVRLRLGRVARKLDHYIE--YGAAVLVLLVCVFG---LAAHWMACIWTISIGDIYIFDE 381
QY 379 ---GIGTRWVY-----DGEQ-----NEYLRCYVAVRTLITIG-GL 411
Db 382 DTKTRNNSWLYQLAMDITGYQYNGSGKWEQSGKNSVYSSLYFTWTSLSVGFN 441
QY 412 PEPQTLFEIVQLNFFSGVFSLSLIGQMRDVTGAATANQNYFRACMDDTIAYMNYSI 471
Db 442 IAPSTDIEKIFAVAIMMIGSLLYATIFGNVTTFIPQMYANTNRYHEMLNSVRDPLKLYQV 501
QY 472 PKLVQKRVRTWYBTWDSQMLDESLLKTLPTTQALADVNFSIISKVDLFKGCDDTQ 531
Db 502 PKGLSERVWDYIVSTWMSRSGIDIEKVLIQICPKDMRADICVHLNRKVPKEHPAFRLASDG 561

QY 532 MIYDMLLKSVLPLPGDFVCKKGEIGKEMVLIKHGEVOVLGGPDGTVLTKAGSVFG 591
Db 562 CLRALAMEFQVHCAPGLDIYHAGESVDSLCFVVSLSLEVI---QDDEVAILKGDVFG 618
QY 592 EI-----SLLAAGGNRRRTANVVAHFANLTLDKTKLQELIVHYPD-----SERILMK-- 640
Db 619 DVFWKEATLA-----QSCANVRALTYCDLHVIKRDALQKLVETAFSHSFNRNLILTYN 673
QY 641 -KAVVLKQ-----KAKTAEATPPRKOLALLFPKKEETPKLFTKLLGGTGKASLARLLK 695
Db 674 LRKIVFRKISDVKREEMRKNEAPLIPDPHVRRLF----- 714
QY 696 REQAQKENSEGEGEENEDKQENEDKQENEDKQENEDKQENEDKQREPEKPLDRPE 755
Db 715 -QRFROQKEARLAAERGRDLDDLDEKGSVLTEHSHHGLAKASVVTVRESPTVPAFPA 773
QY 756 CTASPIAVEEPHVSVRTVLPRTGTSRQSLIISMAPSAEG 794
Db 774 AAA-----PAGLDHARL---QAPGAG 792
RESULT 9
US-09-694-777A-22
; Sequence 22, Application US/09694777A
; Patent No. 6638736
; GENERAL INFORMATION:
; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL
; APPLICANT: STUHRER, WALTER
; APPLICANT: BECKH, SYNNOVE
; APPLICANT: BRUGEMANN, ANDREA
; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO
; APPLICANT: PEREZ, ARACELI SANCHEZ
; APPLICANT: WESELOH, RUDIGER
; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: MPG-8
; CURRENT APPLICATION NUMBER: US/09/694,777A
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: PCT/EP99/02695
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EP 98 10 7268.9
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 987
; TYPE: PRT
; ORGANISM: Bovine sp.
US-09-694-777A-22

Query Match 9.2%; Score 349; DB 4; Length 987;
Best Local Similarity 19.8%; Pred. No. 5.9e-22;
Matches 132; Conservative 114; Mismatches 260; Indels 160; Gaps 23;
QY 221 WLLVTLAYNWCNFIPLRLVFPY-----QTADNHYWLIADIICDIILYDML-----F 270
Db 222 WIIILITFT-----AIIVPYNVSFKTRQNNVAVLWVDSIVDVIFLVDIVLNFHTTF 273
QY 271 IOPRLQFVRGGDIIVDSNELRKHRTSTKFOLDVASIIPEDICYLF----- 316
Db 274 VGP-----AGEVISDPKLIEMNY-LKTFWVIDLLSCLPYDVINAFENVDEVSAPMGDPG 326
QY 317 -FGF-----NPMFRANRMLKVTSP-----EFNHLESIMDKATYIRVIR 355
Db 327 KIGADQIPPLEGREGSQGISLSSKVVRLRLGRVARKLDHYIE--YGAAVLVLLVC 384
QY 356 TTGYLLFFLHINACVYTWASNYE-----GIGTRWVY-----DGEQ----- 391
Db 385 VFG---LAAHWMACIWTISIGDIYIFDEDTKTRNNSWLYQLAMDITGYQYNGSGKWE 441
QY 392 -----NEYLRCYVAVRTLITIG-GLPEPQTLFEIVQLNFFSGVFSLSLIGQMRDV 444
Db 442 GPKNSVYISSLYFTWTSLSVGFNIGAPSTIEKIFAVAIMMIGSLLYATIFGNVTTI 501

Db 327 KVVRLRLGRVARKLDHYIE--YGAALVLLVCFVFG-----LAAHMWACIWIYIGDIYFDE 381
Qy 379 ---GIGTTRWVY-----DDEG-----NEYLRCYVWAVRTLITIG-GL 411
Db 382 DTKTIRNNWLYQLAMDIGTPYQFNGSGKWEKGSXNVYISSLYFTWTSLSVGFN 441
Qy 412 PEPOTLFEIVFOLLNFFSGVFFSSLIQMRDVI GAATANQNYFRACMDDTIAYMNNYSI 471
Db 442 IAPSTDIEKIFAVAIMIGSLLYATIFGNVTTFIQQVYANTNRYHEMLNSVRDFLKYQV 501
Qy 472 PKLVQKVRWYETWDSQRMDESLLKTLPTVQLALADVNFISIISKVDLFGKCDTQ 531
Db 502 PKGLSERVMDYIVSTWSMRGIDTEKVLQICPKDMRADICVHLNRKVKFKEHPAFRLASDG 561
Qy 532 MIYDMLLRKSLVLYPGDFVCKKGEIKEMYIIKHGEVQVLCGPDGTKVLTILKAGSVFG 591
Db 562 CLRALAMEFQTVHCAPGDLIYHAGESVDSLFCFVSGSLEVI---QDDEVAALLKGDVFG 618
Qy 592 EI-----SLLAAGGNRRTANVAHGFANLLTLDKKTLOEILVHYPD-----SERILMK-- 640
Db 619 DVFWKEATLA-----QSCANVRALTYCDJHVIRKDALQKVFYAFSHFSFRNLITYN 673
Qy 641 -KARVLLKQ-----KAKTABATPRKDLALLFPKKEETPKLFTLLGGTGKASLARLLKLK 695
Db 674 LRKGIIVFRKISDVKREEREMKKEAPLILPPDHPVRLF----- 714
Qy 696 REQAQKXENSEGEGEENEDKOKENEDKOKENEDKOKENEDKOGRE-PEEKPLDRP 754
Db 715 -QRFQOKEARLAAERGGRLDDL-----DVEKGNVLTEHASANHS 754
Qy 755 ECTASPIAVEEP 767
Db 755 LVKASVTVRES 767

RESULT 12
US-09-694-777A-3
; Sequence 3, Application US/09694777A
; Patent No. 6638736
; GENERAL INFORMATION:
; APPLICANT: PABLO-FERNANDEZ, LUIS ANGEL
; APPLICANT: STUHRER, WALTER
; APPLICANT: BECKH, SYNNOVE
; APPLICANT: BRUGEMANN, ANDREA
; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO
; APPLICANT: PEREZ, ARACELI SANCHEZ
; APPLICANT: WESELOH, RUDIGER
; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: THEREOF
; CURRENT FILING DATE: 2000-10-23
; PRIOR FILING DATE: 1999-04-21
; PRIOR FILING DATE: 1999-04-21
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 962
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-694-777A-3

Query Match 8.2%; Score 345.5; DB 4; Length 962;
Best Local Similarity 19.9%; Pred. No. 1.2e-21;
Matches 122; Conservative 121; Mismatches 237; Indels 133; Gaps 22;
Qy 221 WLLVTLAYNWCWFLRLVFPY-----QTADNHYWLIADIICDIYVDMLE-----F 270
Db 222 WLLILFTY-----AILVPYNVSKTRQNNVAVLWVDSIVDVIFLVDIVLNFHTTF 273

Qy 271 IQRLQFVRGGDIIVDSNELRKHRTSTKFDLVASIIIPFIDICYLF-----FGNPMFRAN 326
Db 274 VGB-----AGEVISDPKLRIMY-IKTFWVIDLLSCLPYDVINAENFVDEGSISSFLSS 326
Qy 327 RMLKXYSF-----PEFNHLESIMDKAYIRVIRTTGTVLLFILLHINACVYWASNYE----- 378
Db 327 KWVRLRLGRVARKLDHYIE--YGAALVLLVCFVFG-----LAAHMWACIWIYIGDIYFDE 381
Qy 379 ---GIGTTRWVY-----DDEG-----NEYLRCYVWAVRTLITIG-GL 411
Db 382 DTKTIRNNWLYQLAMDIGTPYQFNGSGKWEKGSXNVYISSLYFTWTSLSVGFN 441
Qy 412 PEPOTLFEIVFOLLNFFSGVFFSSLIQMRDVI GAATANQNYFRACMDDTIAYMNNYSI 471
Db 442 IAPSTDIEKIFAVAIMIGSLLYATIFGNVTTFIQQVYANTNRYHEMLNSVRDFLKYQV 501
Qy 472 PKLVQKVRWYETWDSQRMDESLLKTLPTVQLALADVNFISIISKVDLFGKCDTQ 531
Db 502 PKGLSERVMDYIVSTWSMRGIDTEKVLQICPKDMRADICVHLNRKVKFKEHPAFRLASDG 561
Qy 532 MIYDMLLRKSLVLYPGDFVCKKGEIKEMYIIKHGEVQVLCGPDGTKVLTILKAGSVFG 591
Db 562 CLRALAMEFQTVHCAPGDLIYHAGESVDSLFCFVSGSLEVI---QDDEVAALLKGDVFG 618
Qy 592 EI-----SLLAAGGNRRTANVAHGFANLLTLDKKTLOEILVHYPD-----SERILMK-- 640
Db 619 DVFWKEATLA-----QSCANVRALTYCDJHVIRKDALQKVFYAFSHFSFRNLITYN 673
Qy 641 -KARVLLKQ-----KAKTABATPRKDLALLFPKKEETPKLFTLLGGTGKASLARLLKLK 695
Db 674 LRKGIIVFRKISDVKREEREMKKEAPLILPPDHPVRLF----- 714
Qy 696 REQAQKXENSEGEGEENEDKOKENEDKOKENEDKOKENEDKOGRE-PEEKPLDRP 754
Db 715 -QRFQOKEARLAAERGGRLDDL-----DVEKGNVLTEHASANHS 754
Qy 755 ECTASPIAVEEP 767
Db 755 LVKASVTVRES 767

RESULT 13
US-09-358-383C-27
; Sequence 27, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT FILING DATE: 1999-07-21
; PRIOR FILING DATE: 1999-07-21
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: domain
US-09-358-383C-27

Query Match 8.1%; Score 344; DB 4; Length 170;
Best Local Similarity 37.9%; Pred. No. 1.1e-22;
Matches 64; Conservative 33; Mismatches 58; Indels 14; Gaps 2;
Qy 365 HINACVYVWASNYEGIGTTRWY-----DDEGNYLCYVWAVRTLITIG-G 410
Db 1 HNNACLYVWISYKYGFGSDAWYGVNKNPNHWSIVTDNFGROYCYCFWSTLTLTIGOE 60
Qy 411 LPEPOTLFEIVFOLLNFFSGVFFSSLIQMRDVI GAATANQNYFRACMDDTIAYMNNYS 470

ORGANISM: Mus sp.
US-09-694-777A-23

Query Match 7.9%; Score 336; DB 4; Length 989;
Best Local Similarity 19.7%; Pred. No. 8.5e-21;
Matches 126; Conservative 113; Mismatches 242; Indels 158; Gaps 23;

Qy	221	WLLVTLAYNNWCWFIPLRLVPFY-----QTADNIHYWLIADIICDIIYLYDML-----F	270
Db	222	WIIILITFTY-----AIIYPYVVSFKTRQNNVAVLVDSIVDVIPLVDIVLNFHTTF	273
Qy	271	IQPRLOFVGGDIIVDSNLRKHRTSTKFDLVASIIIFDICYLP-----	316
Db	274	VGP-----AGEVISDPKLRMNY-LKTWFIIDLLSCLPYVINAFENVDEVSAFMDGEG	326
Qy	317	-PGF-----NPMFRANMLKVTSPF-----EFNHLESIMDKAYIYRVIR	355
Db	327	KIGFADQIPPLEGRESQGISLFSLLKVVRLRLGRVARKLDHYIE--YGAIVLVLC	384
Qy	356	TTGYLLFILHINACVYVWASNYE-----GIGTTRWVY-----DGEG-----	391
Db	385	VFG---LAAHWMACIWSYIGDYEIFDEDTKTIRNNSWLYQLALDICTPYQFNSSGSGKWE	441
Qy	392	-----NEYLRCYVAVRTLTITIG-GLPEPQTLFEIVFQLLNFFSGVFVFSLLIGOMRDV	444
Db	442	GPSKNSVIISLYFTMTSLTSVGFGNIAPISTDIKIFAVAIMIGSLIYATIFGNVTI	501
Qy	445	IGAATANQNYFRACMDDTIAYMNNYSIPKLIVQKRVETWYETWDSQRMDESLLKTLFT	504
Db	502	FOQWYANTNRYHEMLNSVRDFLKLQVPKGLSERVMDYIVSTWSMRGIDTEKVLQICPK	561
Qy	505	TVQLALAIADVNSIIISKVDLPKGCDDTQMIYDMLRLKSLVLYLPQDFVCKKGEIGKEMYII	564
Db	562	DMRADICVHLNRKVFKEHPAFRLASDGLRALAMEFQTVHCAPGDIIYHAGESVDSLCPV	621
Qy	565	KHGEVOVLGGPDGTVLVTLKAGSVFGEI-----SLLAAGGGRRTANVVAHGAFANLLTLD	620
Db	622	VSGSLEVI---QDDEVVAIIKGQDVGDFVWKEATLA---QSCANVRALTYCDLHLVIK	673
Qy	621	KKTLOEILVHYPD-----SERILMK---KARVLLKQ-----KAKTAAATPPKDLALLPPP	668
Db	674	RDALQKVLFEYTAFSHSFSRNLITVNLKRIIVFRKISDVKREEBEEMKRNKNEAPLILPP	733
Qy	669	KEETPKLPKTLIGGTGKASLARLLKLRQAAOKKENSEGEGEKGKEDKQKEDKQK	728
Db	734	DHPVRRLF-----QFRQCKEARLAERGGRRDLDLDVE-----	767
Qy	729	ENEDKKGKEDKOKGREPEEKPLDRPECTASPIAVEEEP	767
Db	768	---KGNALTDHTSANHGLAK-----ASVTVRESPP	794

Search completed: June 21, 2004, 10:08:25
Job time : 26 secs

This Page Blank (uspto)

Sequence 4, Appli
Sequence 18, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 17, Appli
Sequence 7, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 16, Appli
Sequence 74, Appli
Sequence 74, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 12, Appli
Sequence 25, Appli
Sequence 3, Appli
Sequence 2323, Ap
Sequence 31, Appli
Sequence 6, Appli

ALIGNMENTS

RESULT 1

```

US-10-189-507-11
; Sequence 11, Application US/10189507
; Publication No. US20030228633A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PRONIN, ALEXEY
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: SERVANT, GUY
; APPLICANT: CALLAMARAS, NICHOLAS
; TITLE OF INVENTION: EXPRESSION OF F
; TITLE OF INVENTION: NUCLEOTIDE GAT
; TITLE OF INVENTION: CELLS AND USE
; TITLE OF INVENTION: SMELL MODULATO
; FILE REFERENCE: 078003-0291567
; CURRENT APPLICATION NUMBER: US/10/1
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303,14
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337,15
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-507-11

```

Query Match 21.4%; Score 906; DB 15; Length 237;
Best Local Similarity 72.8%; Pred. No. 9.6e-62;
Matches 171; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

Qy 417 LFEIVFOLLNPFSGVFVFSLLIGOMRDVIGAAATANQYFRACMDDTIAYNNYISIPKLQV 476

QY 417 LFEIVFQLNFFSGVFFSSLIQMRDVTGAATANQVFRACMDDTIAYVNNYSIPKLIVQY

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

QM protein - protein search, using sw model

Run on: June 21, 2004, 10:07:22 ; Search time 49 Seconds
(without alignments)
4661.056 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFSLTKVKNVKPIGENNEN.....PSAEGGSEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of bits satisfying chosen parameters: 1163542

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database : Published Applications AA: *

1: /cgn2_6/prodata1/pubpaa/us07_PUBCOMB.pcp.*
2: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pcp.*
3: /cgn2_6/prodata1/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/prodata1/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/prodata1/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/prodata1/pubpaa/CTUS_PUBCOMB.pcp.*
7: /cgn2_6/prodata1/pubpaa/US08_NEW_PUB.pcp.*
8: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/prodata1/pubpaa/US09A_PUBCOMB.pcp.*
10: /cgn2_6/prodata1/pubpaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/prodata1/pubpaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/prodata1/pubpaa/US09_NEW_PUB.pcp.*
13: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pcp.*
14: /cgn2_6/prodata1/pubpaa/US10_PUBCOMB.pcp.*
15: /cgn2_6/prodata1/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/prodata1/pubpaa/US10_NEW_PUB.pcp.*
17: /cgn2_6/prodata1/pubpaa/US60_NEW_PUB.pcp.*
18: /cgn2_6/prodata1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	906	21.4	237	15	US-10-188-507-11	Sequence 11, Appl
2	902	21.3	237	15	US-10-188-507-1	Sequence 7, Appl
3	850	20.1	694	10	US-09-842-758-75	Sequence 75, Appl
4	850	20.1	694	12	US-10-174-333-75	Sequence 75, Appl
5	850	20.1	694	14	US-10-345-680-26	Sequence 26, Appl
6	829	19.6	663	14	US-10-039-677-16	Sequence 16, Appl
7	825.5	19.5	664	14	US-10-039-677-24	Sequence 24, Appl
8	820.5	19.4	664	14	US-10-039-677-2	Sequence 2, Appl
9	820	19.4	732	10	US-09-842-758-73	Sequence 73, Appl
10	820	19.4	732	12	US-10-174-333-73	Sequence 73, Appl
11	820	19.4	732	14	US-10-039-677-15	Sequence 15, Appl
12	819.5	19.4	664	9	US-09-735-927-2	Sequence 2, Appl
13	819.5	19.4	664	14	US-10-034-843-2	Sequence 2, Appl
14	819.5	19.4	664	14	US-10-168-651-7	Sequence 7, Appl
15	819.5	19.4	664	14	US-10-114-153-18	Sequence 18, Appl

Db 1 LFEIVFOLLNFTGTFVAFSVMIGQMRDVGAAATAGCTYRSCMDSTVKYMMFYKIPKSVQ 60
 QY 477 KRVRTWYETWDSQRMDESDLLKTLPTTVQALALADVNFSTISKVDLFKGCDDTQMIDYM 536
 Db 61 NRKVTWYETWDSQRMDESDLLKTLPTTVQALALADVNFSTISKVDLFKGCDDTQMIDYM 120
 QY 537 LLRLKSVLYLPDGFVCKKGEIKEMVYIIKHGEVQVLGPDGTVKVLVTLKAGSVFGEISLL 596
 Db 121 LKRLSVVLYLPDGFVCKKGEIKEMVYIIKHGEVQVLGPDGTVKVLVTLKAGSVFGEISLL 180
 QY 597 AAGGNRRRTANVVAHGTFANLLTLDKKTQELVHYPDSERILMKKARVLLKQAK 651
 Db 181 AVGGNRRRTANVVAHGTFANLLTLDKKTQELVHYPDSERILMKKARVLLKQAK 235

RESULT 2

US-10-189-507-7
 ; Sequence 7, Application US/10189507
 ; Publication No. US20030228633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOLLER, MARK
 ; APPLICANT: XU, HONG
 ; APPLICANT: STASZEWSKI, LENA
 ; APPLICANT: MOYER, BRYAN
 ; APPLICANT: PRONIN, ALEX
 ; APPLICANT: ADLER, JON ELLIOT
 ; APPLICANT: SERVANT, GUY
 ; APPLICANT: CALLAMARAS, NICHOLAS
 ; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
 ; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
 ; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
 ; TITLE OF INVENTION: SMELL MODULATORS
 ; FILE REFERENCE: 078003-0291567
 ; CURRENT APPLICATION NUMBER: US/10/189,507
 ; CURRENT FILING DATE: 2003-02-12
 ; PRIOR APPLICATION NUMBER: 60/303,140
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 60/337,154
 ; PRIOR FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 237
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-10-189-507-7

Query Match 21.3%; Score 902; DB 15; Length 237;
 Best Local Similarity 72.3%; Pred. No. 2e-61;
 Matches 170; Conservative 30; Mismatches 35; Indels 0; Gaps 0;
 QY 417 LFEIVFOLLNFTGTFVAFSVMIGQMRDVGAAATAGCTYRSCMDSTVKYMMFYKIPKSVQ 476
 Db 1 LFEIVFOLLNFTGTFVAFSVMIGQMRDVGAAATAGCTYRSCMDSTVKYMMFYKIPKSVQ 60
 QY 477 KRVRTWYETWDSQRMDESDLLKTLPTTVQALALADVNFSTISKVDLFKGCDDTQMIDYM 536
 Db 61 NRKVTWYETWDSQRMDESDLLKTLPTTVQALALADVNFSTISKVDLFKGCDDTQMIDYM 120
 QY 537 LLRLKSVLYLPDGFVCKKGEIKEMVYIIKHGEVQVLGPDGTVKVLVTLKAGSVFGEISLL 596
 Db 121 LKRLSVVLYLPDGFVCKKGEIKEMVYIIKHGEVQVLGPDGTVKVLVTLKAGSVFGEISLL 180
 QY 597 AAGGNRRRTANVVAHGTFANLLTLDKKTQELVHYPDSERILMKKARVLLKQAK 651
 Db 181 AVGGNRRRTANVVAHGTFANLLTLDKKTQELVHYPDSERILMKKARVLLKQAK 235

RESULT 3

US-09-842-758-75
 ; Sequence 75, Application US/09842758
 ; Publication No. US20030083244A1
 ; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A. M.
 ; APPLICANT: Fernandes, Elma R.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Padicaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Edward, Szekeres S.
 ; APPLICANT: Alsodbrook II, John P.
 ; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-783
 ; CURRENT APPLICATION NUMBER: US/09/842,758
 ; CURRENT FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 60/200,158
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/200,613
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,780
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/201,006
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,007
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,236
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,238
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,186
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,474
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/201,508
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/220,591
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: 60/232,678
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: 60/263,217
 ; PRIOR FILING DATE: 2001-01-22
 ; PRIOR APPLICATION NUMBER: 60/265,160
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 75
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-842-758-75

Query Match 20.1%; Score 850; DB 10; Length 694;
 Best Local Similarity 30.0%; Pred. No. 9.7e-57;
 Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;
 QY 27 NEEGSHPNQSQQTAAQENKGEKSLKSTPVTSEPHNTNQDKLSKNSSGDLTNP 86
 Db 5 NTQYSHPS-----RTHLKVK-----TSORDLNRAENGLSRAHSSEETS-- 43
 QY 87 DPQNAEPTGTVPQKEMDPKGEKSPQNPKPAPVINEYADALQHLNVLKVRQRTALY 146
 Db 44 ---SVLQP-GIAMEYTRGLADSGQSGFTGQ-----GIARLRLIFLLERWAARH 87

```

QY 147 KKKLVEGDSSP-----EASPTAKPTAVPPVKESDDKPTHEHYRLLMFKVKMPL 197
Db 88 VHQDQGPSDFPRFGAELKEVSSQESNAQAVGQEPADRG-----RSAM-----PL 136
QY 198 -----TEYLKRIKLPNSI-DSYTDRLYLMLLTLVLAWNWCWPIPLRLVPYQT 246
Db 137 AKCNTNTSNTTEEEKTKKDAIVDPSSNLYRWLTAIPVFNWYLLICRACFDELQ 196
QY 247 ADNIHWLIADICDIILYDMLFIQPRLOFVRGGDIIVDSNELRKHVYRTSTKFDLDVAS 306
Db 197 SEYLMWLVDYADVLVLDVL-VRAATGFLQGLMVDSTNRLWQHXYTKTFQKLDVLS 255
QY 307 IIPFDICYLFFGFGN-PMFRANRMLKXTSPFENHLSIMDKAYIRVIRITGYLLFILH 365
Db 256 LVPTDLAYLVKVTGYVEYFENRLLKFSRLEFFDRTETRTNYPNMFRIGNLVLYLIIH 315
QY 366 INACVYVWASNYEGIGTRWVYDG-----EGNEYLRCYVWAVRVLITIGLPPQTL 417
Db 316 WNACIYFAISKFGTDSWVYFNISIPBHGRLSRKYISLYWSTLTTLTIGETPPVKD 375
QY 418 FEIVFOLLNFFSGVFFVSSLIGOMRDVIGAATANQNYFRACMDTIAYNNYSIPKLVK 477
Db 376 EYLVFVVVDPLVGLVLIFAIVGVGSMISNNWASRAEFQAKIDSIKQYMQFRKVTKDLET 435
QY 478 RVRTWYETWDSQRMDESDLLKTLPTTQVLALADVNFISIISKVDLFKGCQTMLYDML 537
Db 436 RVIRWFDYLWANKTKVDEKEVLSLDPKLAETAINVHLDLTKKRIPOCEAGLLVELV 495
QY 538 LRLKSLVLYLPGDFCKYGEIGKEMYYIKHGEVQVGLGPDGKTVLTKAGSVFGEISILA 597
Db 496 LKLRPTVFSGDYICKGDIKGEMYLINECKLAVV-ADGGVTFVVLSDGSYFGEISILN 554
QY 598 AGG---GNRRTANVVAHGFANLITLTKTLOBLVHYDPDSERILMKAR-VLLKQK---A 650
Db 555 IKGSKGNRRNTANIRSIGYDLFCLSKDLMEALTEYPEAKKALEEKGRIKMDNLIDE 614
QY 651 KTEATPPKDLALLFPKZETPKLFKTLGLGGTGKASLARLL-----KLKREOAAQK 702
Db 615 ELAPAGADPKDL-----EKVEQLGSSL--DTLQTFALLAEYNATQMKQRISQLE 666
QY 703 KENSEGEE---EGKENEDKQKXENEDKQK 728
Db 667 SQVKGKGDPLADGEVPGDATK-TEDKQQ 694

```

RESULT 4

```

US-10-174-333-75
; Sequence 75, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zehusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine B.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li

```

```

; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-174-333-75

```

```

Query Match 20.1%; Score 850; DB 12; Length 694;
Best Local Similarity 30.0%; Pred. No. 9.7e-57;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGHPNSQSOQTAAQENKGEKSLTKSPVTSSEPHNTNIQKLSKQSSGDLTNP 86
Db 5 NTQYSHPS-----RTHLVK-----TSRDLNEAENGLSRAHSSSETS-- 43
QY 87 DPONAAEPTGVPEQKEMDPGKGNPSQNKPPAAPVINEYADAOHLNVLKMRORTALY 146
Db 44 ---SVLQP-GIAMEYTRGLADSGGSGFTGQ-----GIARLSLIFLLRWAARH 87
QY 147 KKKLVEGDSSP-----EASPTAKPTAVPPVKESDDKPTHEHYRLLMFKVKMPL 197
Db 88 VHQDQGPSDFPRFGAELKEVSSQESNAQAVGQEPADRG-----RSAM-----PL 136
QY 198 -----TEYLKRIKLPNSI-DSYTDRLYLMLLTLVLAWNWCWPIPLRLVPYQT 246
Db 137 AKCNTNTSNTTEEEKTKKDAIVDPSSNLYRWLTAIPVFNWYLLICRACFDELQ 196
QY 247 ADNIHWLIADICDIILYDMLFIQPRLOFVRGGDIIVDSNELRKHVYRTSTKFDLDVAS 306
Db 197 SEYLMWLVDYADVLVLDVL-VRAATGFLQGLMVDSTNRLWQHXYTKTFQKLDVLS 255
QY 307 IIPFDICYLFFGFGN-PMFRANRMLKXTSPFENHLSIMDKAYIRVIRITGYLLFILH 365
Db 256 LVPTDLAYLVKVTGYVEYFENRLLKFSRLEFFDRTETRTNYPNMFRIGNLVLYLIIH 315
QY 366 INACVYVWASNYEGIGTRWVYDG-----EGNEYLRCYVWAVRVLITIGLPPQTL 417
Db 316 WNACIYFAISKFGTDSWVYFNISIPBHGRLSRKYISLYWSTLTTLTIGETPPVKD 375
QY 418 FEIVFOLLNFFSGVFFVSSLIGOMRDVIGAATANQNYFRACMDTIAYNNYSIPKLVK 477
Db 376 EYLVFVVVDPLVGLVLIFAIVGVGSMISNNWASRAEFQAKIDSIKQYMQFRKVTKDLET 435
QY 478 RVRTWYETWDSQRMDESDLLKTLPTTQVLALADVNFISIISKVDLFKGCQTMLYDML 537
Db 436 RVIRWFDYLWANKTKVDEKEVLSLDPKLAETAINVHLDLTKKRIPOCEAGLLVELV 495

```


Db 3 EKANGVKSPANNHHPAIPAKSGD---DHRASSRPOSAADDTSSELQQLAEMDAP 59
QY 108 KEGNSPQKPPAAPVINYA-----DAQHNLVKRMQRTALYKKLVGEGDLSSEA 160
Db 60 QQRGGFRRIARLVGLVREWAYRNFREBPRPDSFLERF-----GPEL 103
QY 161 SPQAKTAPVPVKESDDKPTTHYVRLWFKVKOMPLTEYLKRIKLPSIDSYDRLYLL 220
Db 104 HTVTTQGGKGDGKGEGKTKKFFELF-----VLDPAAGD-WYIR 142
QY 221 WLLLVTL--AYNWCWFIPLRLVFPYQTDADNIHNLADIICDIILYDMLFIQRLQV 278
Db 143 WLFVAMPVLVNW-CLLV-ARACFSDLOKGYIYVWLVDSVYIAD-LFIRLRTGFL 199
QY 279 RGGDIIVDSNELKHYRTSTKFDLVASIIIPEDICYLFFGF-NPMFRANRLKYSFPF 337
Db 200 EQGLLVKDTKKLNDYIHTLQFKLDVASIIPDIIYPAVDIHSPEVRNLLHFAFMFEF 259
QY 338 NHLESIMDKAYIVRVIRITGTYLLFILHINACVYVWASNYEGIGTRVY----DGE--- 390
Db 260 FDTETRTSYNIFRISNLVYIILIIHWNACIYVYAIKSGISGFGVDTWVYVNTIDPEYGY 319
QY 391 -GNEYLRVYVAVRLLITIGLPEPOTLFEIVFOLLNFFSGVFFSSLIQMRDVIGAAT 449
Db 320 LSREYIYCLWSTLTITIGETPPVKDEEYLFVDFLIGLVIFATIVGVNVMISNMN 379
QY 450 ANQNYFRACMDDTIAYMNNYSIPLVQKRVRTWYETWDSQRMDESLLKTLPTTVQLA 509
Db 380 ATRAEPQAKIDAVKHYMQFRKVKSGEAKVIRWFDLWTKNSVDREVLKNIPLAKRAE 439
QY 510 LAIDVNFISIISKVDLFKGCDDTQMIYDMLLKSVLVLPDGVCKKGEGIKEMVYIKHGEV 569
Db 440 IAINVHLSLTKKVRIFQDCBAGLLVELVLKRPQVSPGDIYICRKGDIKEMVYIKHGEV 499
QY 570 QVLGGPDGTVLTVLKAGSVFGEISLLAAG--GNERTANVVAHGFANLLTLDKKTLOE 626
Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNKGKMGNRRTANIRSLGSDLFCLSKDLM 558
QY 627 ILVHYDSEIRILMKARVLLKQAKTAE---ATPPKDLALLFPKKEETPKLTKLLGGT 683
Db 559 AVTEYPAKVLREGRILMKEGLLDENEVAASMEVDV-----QEKLEQLETNM--DT 610
QY 684 GKASLALILKLKREQAAQKENSEGEGEKENEDKOKEN--EDKOKENEDKOKENEDKD 741
Db 611 LYTRFARLL-----AETGAQOKLKQRTITVLETKMKQNNEDSDSGMN 654
QY 742 KGREPEEKP 750
Db 655 SPEPPAEKP 663
RESULT 7
US-10-029-677-24
; Sequence 24, Application US/10029677
; Publication No. US20030096249A1
; GENERAL INFORMATION:
; APPLICANT: Westphal, Ryan S.
; APPLICANT: Feder, John N.
; APPLICANT: Ramanathan, Chandra S.
; APPLICANT: Mintier, Gabriel A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL
; TITLE OF INVENTION: POLYPEPTIDE
; FILE REFERENCE: D0187NP
; CURRENT APPLICATION NUMBER: US/10/029,677
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/257,865
; FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-029-677-24
Query Match 19.5%; Score 825.5; DB 14; Length 664;
Best Local Similarity 29.6%; Pred. No. 7.2e-55;
Matches 218; Conservative 129; Mismatches 284; Indels 105; Gaps 21;
QY 50 EKSLTKSTPTVTSBEPHTNIQDKLSKNXSGDLTTPDQNAABPTQVPEQK--EMDPG 107
Db 3 EKTNGVKSSPANNENHHA--PPAIIKANGKDDHRTSSRPHSAADDDTSSILQRLADYDAP 59
QY 108 KEGNSPQKPPAAPVINYADAQLH-----NLVKRMQRTALYKKLVGEGDLSSEA 160
Db 60 QQRGGFRRIARLVGLVREWAYRNFREBPRPDSFLERF-----GPEL 103
QY 161 SPQAKTAPVPVKESDDKPTTHYVRLWFKVKOMPLTEYLKRIKLPSIDSYDRLYLL 220
Db 104 QTVTTQGGKGDGKGEGKTKKFFELF-----VLDPAAGD-LYYC 142
QY 221 WLLLVTL--AYNWCWFIPLRLVFPYQTDADNIHNLADIICDIILYDMLFIQRLQV 278
Db 143 WLFVAMPVLVNW-CLLV-ARACFSDLOKGYIYVWLVDSVYIAD-LFIRLRTGFL 199
QY 279 RGGDIIVDSNELKHYRTSTKFDLVASIIIPEDICYLFFGF-NPMFRANRLKYSFPF 337
Db 200 EQGLLVKDTKKLNDYIHTLQFKLDVASIIPDIIYPAVDIHSPEVRNLLHFAFMFEF 259
QY 338 NHLESIMDKAYIVRVIRITGTYLLFILHINACVYVWASNYEGIGTRVY----DGE--- 390
Db 260 FDTETRTSYNIFRISNLVYIILIIHWNACIYVYAIKSGISGFGVDTWVYVNTIDPEYGY 319
QY 391 -GNEYLRVYVAVRLLITIGLPEPOTLFEIVFOLLNFFSGVFFSSLIQMRDVIGAAT 449
Db 320 LAREYIYCLWSTLTITIGETPPVKDEEYLFVDFLIGLVIFATIVGVNVMISNMN 379
QY 450 ANQNYFRACMDDTIAYMNNYSIPLVQKRVRTWYETWDSQRMDESLLKTLPTTVQLA 509
Db 380 ATRAEPQAKIDAVKHYMQFRKVKSGEAKVIRWFDLWTKNSVDREVLKNIPLAKRAE 439
QY 510 LAIDVNFISIISKVDLFKGCDDTQMIYDMLLKSVLVLPDGVCKKGEGIKEMVYIKHGEV 569
Db 440 IAINVHLSLTKKVRIFQDCBAGLLVELVLKRPQVSPGDIYICRKGDIKEMVYIKHGEV 499
QY 570 QVLGGPDGTVLTVLKAGSVFGEISLLAAG--GNERTANVVAHGFANLLTLDKKTLOE 626
Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNKGKMGNRRTANIRSLGSDLFCLSKDLM 558
QY 627 ILVHYDSEIRILMKARVLLKQAKTAE---ATPPKDLALLFPKKEETPKLTKLLGGT 683
Db 559 AVTEYPAKVLREGRILMKEGLLDENEVAATSEVDVQEKLEQLETNMTELYTRFG-- 616
QY 684 GKASLALILKLKREQAAQKENSEGEGEKENEDKOKEN--EDKOKENEDKOKENEDKD 739
Db 617 -----RLI-----AETGAQOKLKQRTITVLETKMKQNNEDSDSGMN 648
QY 740 -KDGREPEEKP 754
Db 649 LSDGMNSPELAAADEP 664
RESULT 8
US-10-029-677-2
; Sequence 2, Application US/10029677
; Publication No. US20030096249A1
; GENERAL INFORMATION:
; APPLICANT: Westphal, Ryan S.
; APPLICANT: Feder, John N.
; APPLICANT: Ramanathan, Chandra S.
; APPLICANT: Mintier, Gabriel A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL
; TITLE OF INVENTION: POLYPEPTIDE
; FILE REFERENCE: D0187NP
; CURRENT APPLICATION NUMBER: US/10/029,677
; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US 60/257,865
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-677-2

Query Match 19.4%; Score 820.5; DB 14; Length 664;
 Best Local Similarity 29.5%; Pred. No. 1.7e-54;
 Matches 217; Conservative 129; Mismatches 285; Indels 105; Gaps 21;
 QY 50 EKSLTKTPTVTSEEPHNTIQDKLSKSSGDLTTPQNAAEPTGTVPQK--EMDPG 107
 DB 3 EKTNGVKSPANNHHA---PPAIKANGKDDHTSSRPHSAADDTSSSELQRLADVAP 59
 QY 108 KEGPNSQNKPPAAPVINEYADAQJH-----NLVKRMQRORTALYKXKLVGDLSSPEA 160
 DB 60 CQGRSGFRIRVLVGIIRWANKNPREEPFRDGFLEFR-----GPEL 103
 QY 161 SPQAKTAPVPEKSDKPTHEYVRLWFKVKKMPLTEYLKRIKLPNSIDSYDRLYL 220
 DB 104 QTVTQEGDGKDGKDGKXKPELF-----VLDPAQD-LYYC 142
 QY 221 WLLVTL--AYNNCWFFPLRLVFPYQADNIHWLIADIICDIYLYDMLFIQPRLOFV 278
 DB 143 WLFVAMPVLYNW-CLLV-ARACFSDQKGYLWLVLDVYDVVYIAD-LFIRLRTGFL 199
 QY 279 RGGDIIVDSNLRKHRYSTKFDVASIIPDFCYLFFGF-NPMFRANMLKXTSFEF 337
 DB 200 EGGLEVKTDLRNYHTLOKLDVASIIPDTLIYFAVDIHSPEVFNRLHFAFMFEF 259
 QY 338 NHLESIMDKAYIVRVIRTCYLLFILHINACVYVWASNYEGITRWVY----DGS--- 390
 DB 260 FDRTRTNYPNIFRISNLVLYLVIHWNACIYVAKSIGFGVDTWVYPTNIDPEYGY 319
 QY 391 -GNEYLRYYAVATLTITIGLPPQTLFEIVFOLLNPFSGVFFVSLIQMRDVIGAAT 449
 DB 320 LAREYIYCLWSTLTITIGTPPPVKDEEYLFVDFLIGLVIFATIVGVNGSMISNMN 379
 QY 450 ANQVFRACMDTITAYNNYSIPKLVOKRVETWYETWDSQRMDESDLLKTLPTTVQLA 509
 DB 380 ATRAEFQAKIDAVKHVYMQFRVSKGMEAKVIRWFDYLTWTKTVDEREILKJPAKLRAE 439
 QY 510 LAIDVNFISIISKVDFKCDQTMIDMLRLKSVLYLPGDFVCKKGIGKEMVIIKHGEV 569
 DB 440 IATNVHLSTLKKVRIHFDCEAGLLVELVLKLPQVPSGDIYCRKGDIGKEMVIIKEGKL 499
 QY 570 QVLGGPDGTVLTKAGSVFGEISLLAAG--GNRSTANVAVHGFANLLTLDKTLQES 626
 DB 500 AVV-ADGVQYALLSAGSCFGEISILNIGSKVGNRNTAIRSLGYSDLFCLSKDLMLE 558
 QY 627 ILVHYPDSERILMKARVLLKQAKTAE---ATPPKXDLALLFPPEETPKFXTLLGGT 683
 DB 559 AVTEYPAKVKVLEGRGAILMKGLLDENEVATSMEDVQKLGQLETNMETLYTRFG-- 616
 QY 684 GKASLALLKLRQAQKKNSEEGEKEKEDKQKEN--EDKQKENEKQKENEKED-- 739
 DB 617 -----RL-----ABYTGAAQKLRITVLETRKQKQ-----NEDDY 648
 QY 740 -KDKGREPEEKPLDRP 754
 DB 649 LSDGMNSPELAAADEP 664

RESULT 9
 US-09-842-758-73
 ; Sequence 73, Application US/09842758
 ; Publication No. US20030083244A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vernet, Corine A. M.

; APPLICANT: Fernandes, Elma R
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Boldog, Ferenc L
 ; APPLICANT: Zerhusen, Bryan D
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Tchernyev, Velizar T
 ; APPLICANT: Padigar, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Gangolli, Baha A
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Taupier, Raymond J
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Edward, Szekeres S
 ; APPLICANT: Alsobrook II, John P
 ; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-783
 ; CURRENT APPLICATION NUMBER: US/09/842,758
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 60/200,158
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/200,613
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,780
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/201,006
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,007
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,236
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,238
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,186
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,474
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/201,508
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/220,591
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: 60/232,678
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: 60/263,217
 ; PRIOR FILING DATE: 2001-01-22
 ; PRIOR APPLICATION NUMBER: 60/265,160
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 73
 ; LENGTH: 732
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-842-758-73

Query Match 19.4%; Score 820; DB 10; Length 732;
 Best Local Similarity 28.8%; Pred. No. 2.2e-54;
 Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;
 QY 24 SRNEEGSHPSNQQTQAENKGE-----EKSLTKTPTVTSEEPHNTIQ 70
 DB 32 TKRKWSSGKGTPTMQSTQCETRRAQTFCBSTGHTWMTKSNKGVKSSPANN---HNNHV 88
 QY 71 DKLKSKSSGDLTTPNPQNAAEPTGTVPQK--EMDPGKEGPNPQKPPAAPVINEYA 128
 DB 89 PATIKANGKDESRFSRPSQSAADDTSSSELQRLAEMDAPQRRGGRFIRVLVGVIRQWA 148
 QY 129 -----DAQJHNLVKRMQRORTALYKXKLVGDLSSPEASQTAKTAPVPPVPEKSDKPT 181

```
Db 149 NNFREEARPSFLERFR-----GPELQVTVTQQGDKGDKGDKGT 192
QY 182 EHYRLLMFKVKMPLTEYLKRIKLPNSIDSYDRLYLLMLLVTL--AYNNMCWFIPLR 239
Db 193 KKKFELF-----VLDPAQD-WYRMLFVIAMPVLYNW-CLLV-AR 229
QY 240 LVFPQTADNTHYMLADIICDILYDMLFIQPLQFVRGDDIIVDSNELKHYRTSTX 299
Db 230 ACPSDLQGYFLVWLVDYFSDVVIAD-LFIRLTGFLQGLLVKOPKLRDNYIHTLQ 288
QY 300 FOLDVASIIPEDICYLFFGF-NPMFRANRMLKYTSFFEFNHLESIMDKAYIYVIRTTG 358
Db 289 FKLDVASIIPDILYFAVGHNHPELFRNLLHFAFMFEFDRTEYTRSYNIPRISNLVL 348
QY 359 YLLFILHINACVYKASNYEGITRWY----DGE-----GNEYLRCYVAVRLTIIG 410
Db 349 YILVLIHWNACIYVAISKISGFGVDVTWYVYNTPEYGYLAREYIYCLYSTLTLLTIGE 408
QY 411 LPEPOTLEIVFQNLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYS 470
Db 409 TPPPVKDEEYLFVIFDPLIGVLIPATIVGVNGVSMISNNNATRAEFQAKIDAVKHYMQFRK 468
QY 471 IPKLVQKVRVYETWDSQRMDESLLKLTPTVQLALAIIDVNFPSIISKVDLFKCDT 530
Db 469 VSKEMEAKVIFWFDYLTWNTKKTVDREVLKPLAKRAETAINVHLSTLKKVRFQDCEA 528
QY 531 QMIYDMLLKLKSLYLPDGFVCKGKEIGEMYIINGHEVQVLGGPDGTGKVLVILKAGSVF 590
Db 529 GLVELVLKRPQVSPGDIYCKRGDIKEMYIIEKGLAVV-ADDGVTQVALLSAGSCF 587
QY 591 GRISILLAGG---GNRRANVAVGHANLLDLDKTLQELIYVHPDSEIRIMKARVLLK 647
Db 588 GRISILNTKSGKNGRNTANIRSLGSDLFCLSKDDLMFAVTEYPDARKVLEERBEILM 647
QY 648 QKAKTAE---ATPPPKDALLFPPEKEETPKLFKTLGGTGKASLARLLKLRQEAQKKE 704
Db 648 KXGLLDENEVAASMEVDVQEKLKQLETWNTLYTRFG-----RLJ-----687
QY 705 NSEGEEREGKEDQKEN--EDROKEDNGKNEKDKGRBEPKPLDRP 754
Db 688 ----AEYTAQOKLQXRTVILEVKOKONTE---DDYLSGDMNSPEPAAAEQP 732

RESULT 10
US-10-174-333-73
; Sequence 73, Application US/10174333
; Publication NO. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Cangelli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
```

```
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 73
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; US-10-174-333-73
```

```
Query Match 19.4%; Score 820; DB 12; Length 732;
Best Local Similarity 28.8%; Pred. No. 2.2e-54;
Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;

QY 24 SRNREGSHPSNQSQTTAQENKGE-----EKSLTKTPTVSEPHNIQ 70
Db 32 TKRKWSGKGTPMQSTOCETRRRAQTPCESTGHTWMTKSNVKSPPANN---HNNHV 88
QY 71 DXLSKNSGDLTNPDPQNAAEPTGVPEQK--EMDPGKEGPNSPQKPPAAVINEYA 128
Db 89 PATIKANGKDESRTSRPQSAADDDTSSELQRLAEMDAPQORRGFRIRVLVGIQWA 148
QY 129 -----DAQLNLVVRMRQRTALYKKLVESDLSSEASPTAKTAVPVKESDDKPT 181
Db 149 NNFREEARPSFLERFR-----GPELQVTVTQQGDKGDKGDKGT 192
QY 182 EHYRLLMFKVKMPLTEYLKRIKLPNSIDSYDRLYLLMLLVTL--AYNNMCWFIPLR 239
Db 193 KKKFELF-----VLDPAQD-WYRMLFVIAMPVLYNW-CLLV-AR 229
QY 240 LVFPQTADNTHYMLADIICDILYDMLFIQPLQFVRGDDIIVDSNELKHYRTSTX 299
Db 230 ACPSDLQGYFLVWLVDYFSDVVIAD-LFIRLTGFLQGLLVKOPKLRDNYIHTLQ 288
QY 300 FOLDVASIIPEDICYLFFGF-NPMFRANRMLKYTSFFEFNHLESIMDKAYIYVIRTTG 358
Db 289 FKLDVASIIPDILYFAVGHNHPELFRNLLHFAFMFEFDRTEYTRSYNIPRISNLVL 348
QY 359 YLLFILHINACVYKASNYEGITRWY----DGE-----GNEYLRCYVAVRLTIIG 410
Db 349 YILVLIHWNACIYVAISKISGFGVDVTWYVYNTPEYGYLAREYIYCLYSTLTLLTIGE 408
QY 411 LPEPOTLEIVFQNLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYS 470
Db 409 TPPPVKDEEYLFVIFDPLIGVLIPATIVGVNGVSMISNNNATRAEFQAKIDAVKHYMQFRK 468
QY 471 IPKLVQKVRVYETWDSQRMDESLLKLTPTVQLALAIIDVNFPSIISKVDLFKCDT 530
Db 469 VSKEMEAKVIFWFDYLTWNTKKTVDREVLKPLAKRAETAINVHLSTLKKVRFQDCEA 528
```



```

Db 260 FDRTRTNYPNIPRISNLVLYLVIIHWNACIYYAISKSIGFVGTWVYFNITDPEYGY 319
QY 391 -GNEVLCRYVAVRTLIITIGLPEPQTLFEIVPOLNFFSGVFSSLIQOMRDVIGAT 449
Db 320 LAREVIYCLYNSTLTITIGTTPPVKDEEYLFVDFLIGLVLIATVGNVSGMSNMN 379
QY 450 ANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSORMLDESLLKTLPTTVOLA 509
Db 380 ATRAEFOAKIDAVKHYMQFRKVSQKMEAKVIRWFDYLTWTKTVDEREILKNLPKRAE 439
QY 510 LAIDVNFIIISKVDLFGCDTQMIDMLRLKSVLYLPDGVCKKGIKEMVIIKHGEV 569
Db 440 IAINVHLSTLKKVRIHDCAGLVELVLKRPQVPSFGDYICRKGDIKEMIIKEGL 499
QY 570 QVLGPDGTQKVLVTLKAGSVFGEISLLAAG--GNRTANVVAHGFANLLTLDKKTLOE 626
Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNIGKSGMGNRTANIRSLGVSDFCLSKODLME 558
QY 627 ILVHPDSEIRILMKARVLLKQAKTAE---ATPPKDLALLPPKBEETPKLFTLLGGT 683
Db 559 AVTEYPDRAKVLBERGRIILMKEGLLDENEVATSMEDVQEKLGQLETNMTLYTRFG-- 616
QY 684 GKASLARLLKLRQAAQKENSEGEGEKENEDKOKEN--EDKOKENEDKOKENED-- 739
Db 617 -----RL-----AYTGAQKQKQRTVLETKMKN-----NEDDY 648

RESULT 13
US-10-034-843-2
; Sequence 2, Application US/10034843
; Publication No. US2002011478A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; TITLE OF INVENTION: NO. US2002011478A1el Human Ion Channel Protein and Polynucleotide
; FILE REFERENCE: LEX-0291-USA
; CURRENT APPLICATION NUMBER: US/10/034,843
; CURRENT FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 664
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-034-843-2

Query Match 19.4%; Score 819.5; DB 13; Length 664;
Best Local Similarity 29.5%; Pred. No. 2.1e-54;
Matches 217; Conservative 129; Mismatches 285; Indels 105; Gaps 21;

QY 50 EKSJTKTPTVTSBEPHNIQDKSKNSDGLTNPDPQNAAPCTVPEQK--EWDPG 107
Db 3 EKTNGVSKSPANNHHA---PPAKANGKDDHRTSRPHSAADDDTSSLOQLADVDAP 59
QY 108 KEGNPSQNPQPPAFAVINEYADAOLH-----NLKRMQRQALYKXKLVEGDLSSPEA 160
Db 60 QQGRSGFRIRVLVGLIREWANKNFRPEPRDPSFLERF-----GPEL 103
QY 161 SPQAKTAPVAPVKESDDKPTHEYRLLWFKVKOMPLTEYLKRLPNSIDSTYDRLLYLL 220
Db 104 QTVTTQEGGKGDKGDKGDKGDKKKKFFELF-----VLDPAGD-WYVC 142
QY 221 WLLVTL--AYNWCNCFPIRLVFPYQADNIHYWLIADIICDIILYDMLFTQPSLQFV 278
Db 143 WLFVIAFVPLVNW-CLIV-ARACFSDILQKGYLWLVLDVSDVWIAD-LFIRLRTGFL 199
QY 279 RGGDIIVDSNELRKHRTSTKQFDVASIIPFDICYLFFGFS-NPMFRANRLKYTSFFEF 337

```

```

Db 200 EQGLVKDTKKLRNYHTLQFKLDVASIIPDILYIFAVDIHSPFVFNELLPARMFEP 259
QY 338 NHHLESIMDKAYIYRVIRTTGYLLFIHINACVYVWASNYEGIGTRRWY---DGE--- 390
Db 260 FDRTRTNYPNIPRISNLVLYLVIIHWNACIYYAISKSIGFVGTWVYFNITDPEYGY 319
QY 391 -GNEVLCRYVAVRTLIITIGLPEPQTLFEIVPOLNFFSGVFSSLIQOMRDVIGAT 449
Db 320 LAREVIYCLYNSTLTITIGTTPPVKDEEYLFVDFLIGLVLIATVGNVSGMSNMN 379
QY 450 ANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSORMLDESLLKTLPTTVOLA 509
Db 380 ATRAEFOAKIDAVKHYMQFRKVSQKMEAKVIRWFDYLTWTKTVDEREILKNLPKRAE 439
QY 510 LAIDVNFIIISKVDLFGCDTQMIDMLRLKSVLYLPDGVCKKGIKEMVIIKHGEV 569
Db 440 IAINVHLSTLKKVRIHDCAGLVELVLKRPQVPSFGDYICRKGDIKEMIIKEGL 499
QY 570 QVLGPDGTQKVLVTLKAGSVFGEISLLAAG--GNRTANVVAHGFANLLTLDKKTLOE 626
Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNIGKSGMGNRTANIRSLGVSDFCLSKODLME 558
QY 627 ILVHPDSEIRILMKARVLLKQAKTAE---ATPPKDLALLPPKBEETPKLFTLLGGT 683
Db 559 AVTEYPDRAKVLBERGRIILMKEGLLDENEVATSMEDVQEKLGQLETNMTLYTRFG-- 616
QY 684 GKASLARLLKLRQAAQKENSEGEGEKENEDKOKEN--EDKOKENEDKOKENED-- 739
Db 617 -----RL-----AYTGAQKQKQRTVLETKMKN-----NEDDY 648

RESULT 14
US-10-168-651-7
; Sequence 7, Application US/10168651
; Publication No. US20030171275A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YANG, Junning
; APPLICANT: REDDY, Roopa
; APPLICANT: LAL, Preeti
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Valda
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: YAO, Monique G.
; APPLICANT: GANDHI, Aneeni R.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Parrah A.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0005 PCT
; CURRENT APPLICATION NUMBER: US/10/168,651
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758; 60/181,625
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02; 2000-02-10
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

```

APPLICANT: Guo, Xiaojia
APPLICANT: Gerlach, Valerie

DP 143 WLFVLA MPVLYNW-CLLV-ARACFSDLQKGYYLVWLVDVSDVWYIAD-LFIRLRTGFL 199

AFRICANA: GERRARD, VALERIE

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 17:15:34 ; Search time 10368.6 Seconds
(without alignments)
11299.126 Million cell updates/sec

Title: US-09-855-828-2

Perfect score: 2703

Sequence: 1 cattctctacttaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb.ba:**

2: gb.htg:**

3: gb.in:**

4: gb.om:**

5: gb.ov:**

6: gb.pat:**

7: gb.ph:**

8: gb.pl:**

9: gb.pr:**

10: gb.to:**

11: gb.ats:**

12: gb.sy:**

13: gb.un:**

14: gb.vi:**

15: em.ba:**

16: em.fun:**

17: em.hum:**

18: em.in:**

19: em.mu:**

20: em.om:**

21: em.or:**

22: em.ov:**

23: em.pat:**

24: em.ph:**

25: em.pl:**

26: em.to:**

27: em.ats:**

28: em.un:**

29: em.vi:**

30: em.htg.hum:**

31: em.htg.inv:**

32: em.htg.other:**

33: em.htg.mus:**

34: em.htg.pln:**

35: em.htg.rod:**

36: em.htg.mam:**

37: em.htg.vrt:**

38: em.sy:**

39: em.htgo.hum:**

40: em.htgo.mus:**

41: em.htgo.other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2667.4	98.7	4369	9	AF272900	AF272900 Homo sapi
2	2108.4	78.0	2135	9	AF228520	AF228520 Homo sapi
3	1822.8	67.4	2826	4	AF490511	AF490511 Canis fam
4	1452	53.7	4710	10	MMU243572	AJ243572 Mus muscu
5	577.4	21.4	3025	9	HUMCNCGCB	U15237 Homo sapien
6	577.4	21.4	3408	9	HUMCNCGCA	U15236 Homo sapien
7	577.4	21.4	4033	9	HSU58837	U58837 Human CGMP-
8	577.4	21.4	4382	9	AF042498	AF042498 Homo sapi
9	575.2	21.3	4763	10	BC045114	BC045114 Mus muscu
10	572.2	21.2	3083	4	AF074012	AF074012 Bos tauru
11	572.2	21.2	3090	4	AF074013	AF074013 Bos tauru
12	572.2	21.2	3253	4	BTCNG4CGN	X94707 B.taurus mr
13	572.2	21.2	3290	4	AF074014	AF074014 Bos tauru
14	572.2	21.2	4282	4	BTRPCNGCL	X89636 B.taurus mr
15	569.6	21.1	4238	10	RNCNG41	AJ000496 Rattus no
16	568	21.0	3236	10	RNCNG43	AJ000515 Rattus no
17	568	21.0	3328	10	AF068572	AF068572 Rattus no
18	521.4	19.3	205816	9	AC013751	AC013751 Homo sapi
19	237.4	8.8	2511	3	CEU73476	U73476 caenorhabdi
20	223	8.3	3358	3	BT001439	BT001439 Drosophil
21	217.8	8.1	3099	10	BC046523	BC046523 Mus muscu
22	196.2	7.3	441	10	AF015728	AF015728 Rattus no
23	192.4	7.1	187022	9	AC090572	AC090572 Homo sapi
24	192.4	7.1	189126	2	AC021132	AC021132 Homo sapi
25	187.4	6.9	1709	3	AY060725	AY060725 Drosophil
26	181.2	6.7	2061	4	SSU85404	U85404 Sus scrofa
27	181.2	6.7	2857	9	S42457	S42457 CNCU-rod ph
28	176.8	6.5	2697	4	CFACGMP	X99914 C.familiari
29	176.8	6.5	2717	4	CFU83905	U83905 Canis famil
30	176.4	6.5	2500	9	HUMCGMP	M84741 Human CGMP-
31	175	6.5	201246	10	AL683894	AL683894 Mouse DNA
32	173.6	6.4	2682	4	BTCGMPECH	X51604 B.taurus RN
33	169.8	6.3	1674	9	AF547222	AF547222 Homo sapi
34	169.8	6.3	181804	9	AC107068	AC107068 Homo sapi
35	166.9	6.2	233700	2	AC117107	AC117107 Rattus no
36	166.4	6.2	2297	10	MMU19717	U19717 Mus musculu
37	164.8	6.1	2474	10	MUSCNCG	M84742 Mus musculu
38	162.4	6.0	6312	3	AF091302	AF091302 Limulus p
39	161.4	6.0	58409	10	AL772281	AL772281 Mouse DNA
40	155.6	5.8	2612	5	GGRODCNG	X89599 G.gallus mr
41	152	5.6	2052	10	RNU48803	U48803 Rattus norv
42	150.6	5.6	200535	10	AL671880	AL671880 Mouse DNA
43	150.6	5.6	222930	2	AC099698	AC099698 Mus muscu
44	150.2	5.6	181805	2	AC114445	AC114445 Rattus no
45	150.2	5.6	190000	2	AC007704	AC007704 Homo sapi

ALIGNMENTS

RESULT 1	AF272900	4369 bp	mRNA	linear	PRI 29-AUG-2000
LOCUS	AF272900				
DEFINITION	Homo sapiens cone photoreceptor cyclic nucleotide-gated channel				
ACCESSION	AF272900				
KEYWORDS	Beta subunit (CNGB3) mRNA, complete cds.				
SOURCE	AF272900.1	GI:9247065			
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 4369)				
AUTHORS	Kohl,S., Baumann,B., Broghammer,M., Jagle,H., Sieving,P., Kellner,U., Spegal,R., Anastasi,M., Zrenner,E., Sharpe,L.T. and				

<p>Wissinger, B. Mutations in the CNGB3 gene encoding the beta-subunit of the cone photoreceptor cGMP-gated channel are responsible for achromatopsia (ACHM3) linked to chromosome 8q21 Hum. Mol. Genet. 9 (14), 2107-2116 (2000) 2044632 10958649 PUBMED REFERENCE AUTHORS TITLE JOURNAL SUBMITTED (30-MAY-2000) University Eye Hospital, Molecular Genetics Laboratory, Auf der Morgenstelle 15, Tuebingen D-72076, Germany Location/Qualifiers 1. 4369 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1. 4369 /gene="CNGB3" 47. .2476 /gene="CNGB3" /codon_start=1 /product="cone photoreceptor cyclic nucleotide-gated channel beta subunit" /protein_id="BAF66274.1" /db_xref="GI:9247066"</p>		<p>/translation="MFSLTKVKNKPIGENNENQSRNEBSPNSQOQTAE ENKGEKSLKTSPTVSEEPHTNIQDKSKNSGDLTTPDPQNAEPTGVPEQ EMDPCKEGSPQNPAPVINEYADQLNLRMRQRTALYKKLVGDLSSPEA SPQAKPTAPVPPKESDQKPEHYRLLMFKVKKMPLTEYLKIKLPSNDSVTDRLY LMLLLVLAANNMCRTPLELVFPYOTADNIHMLADIIIDIIYLDMLFQPLQ FVRGDIIVDSNELRKHYRSTKEQLVASIIPEDICILFEFNPFRANRMLKITSF FEFNHLSIMDKATITKIRITGTLFILHINACVYMASNVEGIGTIRWYDGEEN EYLKYVAVRLLITGLPEPTEIFVQLNFFSGVFPVSLIGQMRDVIKAATA NONFRACMDITIAMNYSIPKLVQRVETWYDWSQRLDESLKLTPLTVQL ALADVNFISIKVLDKFGDQTMIDMLRLKSLVLPDGFVCKEIGKEMV1IKH GEVQVLDGPTQKLVTLKAGSVFGEISLLAAGGNRRTANVVAHGFANLLTDKTL QELIVHPDSRILMKARVLLKOKAKTAETPRKDLALLFPKPEETPKLFTLGG TGKSLARLLKKEQAOKENSEGEEBEGKEDKQENEDKQENEDKQENEDK DKGREPEKPLDRECFASPIAVVEEPHVRVLPKRTSRQSLIISMAPSABGSEV LTIEVKEKAKQ"</p>	
<p>Query Match 98.7%; Score 2667.4; DB 9; Length 4369; Best Local Similarity 100.0%; Pred. No. 0; Matches 2668; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>		<p>17 GGCACAGTCATAAATACAGAGGGTTTTCAGAACCACTCAGAGAAGATGTTAAATCGCT 76 1 GGCACAGTCATAAATACAGAGGGTTTTCAGAACCACTCAGAGAAGATGTTAAATCGCT 60 77 GACAAAAGTCAACAGGTGAAGCTTATAGAGAGAACAAATGAGAAAGTCTTCG 136 61 GACAAAAGTCAACAGGTGAAGCTTATAGAGAGAACAAATGAGAAAGTCTTCG 120 137 TCGGAATGAAGAAGCTCTCACCAAGTAATCAGTCTCAGCAAAACACACAGGAAGA 196 121 TCGGAATGAAGAAGCTCTCACCAAGTAATCAGTCTCAGCAAAACACACAGGAAGA 180 197 AAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCACTCCAGTCAAGTCTCAAGAGCC 256 181 AAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCACTCCAGTCAAGTCTCAAGAGCC 240 257 ACACCAACATACAGACAACTCTCCAAAGAAAAATTCCTCTGGAGATCTGACCAACAAA 316 241 ACACCAACATACAGACAACTCTCCAAAGAAAAATTCCTCTGGAGATCTGACCAACAAA 300 317 CCCTGACCTTCAAAATCAGCAGAACCAACTGAAACAGTCCGACGAGAGAAATGGA 376 301 CCCTGACCTTCAAAATCAGCAGAACCAACTGAAACAGTCCGACGAGAGAAATGGA 360 377 CCCCGGGAAGAGAGGTCCAAACAGCCCAACAAAACCAACCGCCCTGACGCTCCTGTTATAAA 436</p>	
<p>ORIGIN</p>		<p>Db 361 CCCCGGGAAGAGAGGTCCAAACAGCCCAACAAAACCAACCGCCCTGACGCTCCTGTTATAAA 420 Qy 437 TGAGTATGCCGATGCCAGCTACAAACCTGGTGAAGAAATGCGTCAAGAACAGCCCT 496 Db 421 TGAGTATGCCGATGCCAGCTACAAACCTGGTGAAGAAATGCGTCAAGAACAGCCCT 480 Qy 497 CTACAGAAAGAAAGTTCGTAGAGGAGATCTCTCTCACCAGGAGCCAGCCCAACAACTGC 556 Db 481 CTACAGAAAGAAAGTTCGTAGAGGAGATCTCTCTCACCAGGAGCCAGCCCAACAACTGC 540 Qy 557 AAAGCCACAGGCTGTACCAACAGTAAAGAAAGAGGATGATAGCCCAACAGAACTACTA 616 Db 541 AAAGCCACAGGCTGTACCAACAGTAAAGAAAGAGGATGATAGCCCAACAGAACTACTA 600 Qy 617 CAGGCTGTGTGGTTCARAGTCAAAAGATGCTTTTAAACAGAGTACTTTAAAGCGAATTA 676 Db 601 CAGGCTGTGTGGTTCARAGTCAAAAGATGCTTTTAAACAGAGTACTTTAAAGCGAATTA 660 Qy 677 ACTTCCAAAACAGCATAGATTACACAGATCGACTCTATCTCTCTGTGGCTCTTCTTGT 736 Db 661 ACTTCCAAAACAGCATAGATTACACAGATCGACTCTATCTCTCTGTGGCTCTTCTTGT 720 Qy 737 CACTCTTGGCTATACCTGAACTGCTGTTTATACACATCGCCCTCGTCTCCCATATCA 796 Db 721 CACTCTTGGCTATACCTGAACTGCTGTTTATACACATCGCCCTCGTCTCCCATATCA 780 Qy 797 AACCGCAGACAAACATACACTACTGGCTTATTCGGACATCATATGTGATATCATCTACT 856 Db 781 AACCGCAGACAAACATACACTACTGGCTTATTCGGACATCATATGTGATATCATCTACT 840 Qy 857 TTATGATATGCTATTATTCACGCCAGACTCCAGTTTGTAAAGAGGAGAGACATAATAGT 916 Db 841 TTATGATATGCTATTATTCACGCCAGACTCCAGTTTGTAAAGAGGAGAGACATAATAGT 900 Qy 917 GCAATTCAATGAGCTTAAGGAAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCG 976 Db 901 GCAATTCAATGAGCTTAAGGAAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCG 960 Qy 977 ATCAATAATACATTTGATATTTGCTACTCTCTCTTTCGGTTAATCCAAATGTTTAGAGC 1036 Db 961 ATCAATAATACATTTGATATTTGCTACTCTCTCTTTCGGTTAATCCAAATGTTTAGAGC 1020 Qy 1037 AAATAGGATGTAAGTACACTTCAATTTTTCGAATTTAATCATCACCTAGAGTCTATAAT 1096 Db 1021 AAATAGGATGTAAGTACACTTCAATTTTTCGAATTTAATCATCACCTAGAGTCTATAAT 1080 Qy 1097 GGACAAAGCATATATCTACAGAGTTTATTCGAACAACTGGATCTTGTGTTTATCTGCA 1156 Db 1081 GGACAAAGCATATATCTACAGAGTTTATTCGAACAACTGGATCTTGTGTTTATCTGCA 1140 Qy 1157 GATTAATGCTGTGTTTATTTACTGGCTTCAAACTAAGAGAAATGCGACTACTAGATG 1216 Db 1141 GATTAATGCTGTGTTTATTTACTGGCTTCAAACTAAGAGAAATGCGACTACTAGATG 1200 Qy 1217 GGTGTATGATGGGAGGAAACGAGATCTCAGAGTGTATTATTATTTGGGAGTTTCAACTTT 1276 Db 1201 GGTGTATGATGGGAGGAAACGAGATCTCAGAGTGTATTATTATTTGGGAGTTTCAACTTT 1260 Qy 1277 AATTACCAATGGTGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTCACCTCTT 1336 Db 1261 AATTACCAATGGTGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTCACCTCTT 1320 Qy 1337 GAATTTTCTGGAGTTTGTCTCCAGTTTAAATTTGTTTGGTCAAGATGAGATGAT 1396 Db 1321 GAATTTTCTGGAGTTTGTCTCCAGTTTAAATTTGTTTGGTCAAGATGAGATGAT 1380 Qy 1397 TGGAGCAGTACAGCCAAATCAGAACTACTCTCCGCGCTCGATGGATGACACCAATGCTA 1456 Db 1381 TGGAGCAGTACAGCCAAATCAGAACTACTCTCCGCGCTCGATGGATGACACCAATGCTA 1440 Qy 1457 CATGAACTTACTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1516 Db 1441 CATGAACTTACTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1500</p>	

(CNGB3) mRNA, complete cds.
AF490511 GI:22023792
AP490511.1
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 2826)
Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M.,
Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.
Canine CNGB3 mutations establish cone degeneration as orthologous
to the human achromatopsia locus ACHM3
Hum. Mol. Genet. 11 (16), 1823-1833 (2002)
JOURNAL
PUBMED
12140185
REFERENCE
2 (bases 1 to 2826)
Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M.,
Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.
Direct Submission
Submitted (05-MAR-2002) Baker Institute, Cornell University,
Hungerford Hill Rd., Ithaca, NY 14853, USA
FEATURES
source
1..2826
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
1..2826
/gene="CNGB3"
25..2373
/gene="CNGB3"
/codon_start=1
/product="cyclic nucleotide gated channel beta subunit"
/protein_id="AA089224.1"
/db_xref="GI:22023793"
/translation="MFKSLTIKGNKVKPRENDENKQDPDPSNPQOQSTROGKNSEN
KSLQKMPVTFEESHAKMDKISEKNSLDLTPNPHCHPTSEKAMSEQKEMETGK
EGLVPSKSLGVPVNEVADOLNLRMRORTWLYKKLAEGDISSEPEASQPTAK
PTAVPSQESNKLKEHYVHILCFKQKMLPEYLKRFELPGSIDSYDRLYLWLL
LVFLAYNNCHLLPLRLVFPYQPDNTHYFIDTDCDIILYCDMLLIQPRLOPIKGG
DIWDVSNELKHRSSTFQDVAWNPFDVFLFFGFNPFVRNKLKLTISFFENH
HLESIMDKAYIVIRTYGLLYLHINACIYYWASDYDEIGSTRWYNGEKNYLRC
YYAVARTLITIGLPEPQTFEIVQLNFPFSGVFPFSSLIQGMQDVIQAATQNNF
RISMDHTISYNTYVSPKQNVNRVRYEYTWDSQRLMDESLDCLTLPVTMLALVD
NLSIIISKVLFGKQDQMIYDMLRLKSVYLPQFVCKKGIGKEMYIIKQGEVQV
LGSDGAQVLTILKAGAVGEI SILLAGRGNRNTANVIAHGFANILTLQKTLQELIV
HYDPSKLLMKKASVLLKKAPATEPTPPKQGLAFPLPPKQETPKFKALLSGTGAG
LTRLKKRQSTQKTSENSEGGKKREYEDKREPFSEKILDSSECRANCIITAEEMP
QSIRRAALPRGTTTQSLIISMAPSAEAGEEVLITIEVKEKAKQ"

Query Match 67.4%; Score 1822.8; DB 4; Length 2826;
Best Local Similarity 83.1%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 347; Indels 100; Gaps 6;
39 GTTTTCAGAACCCCTCAGAGAAGATGTTTAAATCGCTGAC---AAAAGTCACAAGGTG 95
Db 1 GTTTTCAGAACCCCTCAGAGAAGATGTTTAAATCACTGACAAATAAATCCAAAGGTG 60
96 AAGCCTATAGAGAGACAAATGAGATGAACAAGTTCTCGTCGGAATGAGAGGCTCT 155
Db 61 AAGCCTAGAGAGAGATGATGAGAAATAACAAGATCCTGAT----- 102
156 CACCCAAGTATCATCTCAGCAAAACCACAGCAGAGAGAAACAAAGGTGAAGAGAA 215
Db 103 ---CCAAGCAATCAGCTCAGCAATCTACAAGCAGGAGAGAAACAAAGTGAATAA 159
216 TCTCTCAAAACCAAGTCACTCAGTCAAGTCAAGTCAAGAGCCACACCAACATCAAGAC 275
Db 160 TCTCTCAAAACCAAGTCACTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 219
276 AAACCTCTCCAGAGAAATTCCTCTGGAGATCTGACCAACAAACCTGACCCCTCAAAATGCA 335
Db 220 AAATCTCCAGAGAAATTCCTCTGAGAGATCTGAGAGATCTGAGAGATCTGAGAGAT 279

ORIGIN
Query Match 67.4%; Score 1822.8; DB 4; Length 2826;
Best Local Similarity 83.1%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 347; Indels 100; Gaps 6;
39 GTTTTCAGAACCCCTCAGAGAAGATGTTTAAATCGCTGAC---AAAAGTCACAAGGTG 95
Db 1 GTTTTCAGAACCCCTCAGAGAAGATGTTTAAATCACTGACAAATAAATCCAAAGGTG 60
96 AAGCCTATAGAGAGACAAATGAGATGAACAAGTTCTCGTCGGAATGAGAGGCTCT 155
Db 61 AAGCCTAGAGAGAGATGATGAGAAATAACAAGATCCTGAT----- 102
156 CACCCAAGTATCATCTCAGCAAAACCACAGCAGAGAGAAACAAAGGTGAAGAGAA 215
Db 103 ---CCAAGCAATCAGCTCAGCAATCTACAAGCAGGAGAGAAACAAAGTGAATAA 159
216 TCTCTCAAAACCAAGTCACTCAGTCAAGTCAAGTCAAGAGCCACACCAACATCAAGAC 275
Db 160 TCTCTCAAAACCAAGTCACTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 219
276 AAACCTCTCCAGAGAAATTCCTCTGGAGATCTGACCAACAAACCTGACCCCTCAAAATGCA 335
Db 220 AAATCTCCAGAGAAATTCCTCTGAGAGATCTGAGAGATCTGAGAGATCTGAGAGAT 279

Query Match				53.7%; Score 1452; DB 10; Length 4710;			
Best Local Similarity				75.4%; Pred. No. 9.4e-269; Indels 91; Gaps 10;			
Matches 1976; Conservative 0; Mismatches 555;							
Qy	19	CACAGTCAATAACAGAGGTTTTCAGAACCACTCAGAGAGAGATGTTTAAATPCGCTGA	78	Db	1030	GAGCAATCGGATATTAAGTATACCTTCTATCTTTGAGTTTAAACCATCACCTGGAGTCTA	1089
Db	40	CAGGTCATATAATCGGAGGTCTTTCAGACTGCTCCTCAGAGAGATGTTAAATCACTGA	99	Qy	1093	TAATGGACAAGACATATATCTACAGAGTTATTCGAACAACTCGATACCTTCTGTTTATTC	1152
Qy	79	C---AAAAGTCAACAGGTGAGGCTATAGAGAGACAAATGAGATGAACAAAGTTCTC	135	Db	1090	TAATGGACAAGACATATATCTACAGAGTATCGGAACAACTCGGCTACTTCTGTTTCTCC	1149
Db	100	CAGTAAATTCACAAAGTGAATCCCATGGAGGGAGATGGAGAGAACTCT-----	153	Qy	1153	TCACATTAATCCCTGTGTGTTTATTAATCTGGGCTTCAAACTATGAAGGAATTTGGCACTACTA	1212
Qy	136	GTCGGAATGAAGAGGCTCTCACCAAGTAACTAGTCTCAGCAAAACACAGACAGGAAG	195	Db	1150	TCACATTAATCCCTGTGTGTTTATTAATCTGGGCTTCAAGCTATGAAGGAATTTGGCTCACTA	1209
Db	154	-----GCCCAACCTGAGAGCTCTTCTCAGCCAAACCATAGCAGAGGAG	198	Qy	1213	GATGGGTGATCATGGGAAGGAAAACGAGTATCTCAGATGTTTATTTATTTATTTGGGAGTTCCAA	1272
Qy	196	AAAAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCAGTCACTGCTCTGAGAGC	255	Db	1210	AATGGGTCTATAATGGTGAAGGCAACAAGTATCTCGATGCTTTTATTTGGGAGTTCCAA	1269
Db	199	ACAAACCAAGTGAAGAAAGACCTCTGAGGAGCAGG---ACACCAATCACATTTGAAAGT	255	Qy	1273	CATTAAATACCATTTGGTGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTCACAC	1332
Qy	256	CACACACACATACAAGACAACTCTCCAAGAAAATTTCTCTGGAGATCTGACCACAA	315	Db	1270	CTTTAAATTAATCTCGGGGCTTCCAGAGCCACAGACTCATTTGAAATTTGTTTTTCAAT	1329
Db	256	CACACAGGAA---AGAAGACACAGACTGGGGAATACTCTCAGAGATTTCAACCCAA	312	Qy	1333	CTTGAATTTTTTCTCGAGTTTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGAGATG	1392
Qy	316	ACCTGACCTTCAAAATGACAGACAACTGGAACAGTGGCCAGAGCAGAGAAATGG	375	Db	1330	CTTGAATTTTTTCTCGGGTTTTTGTGTTCTCCAGCTTAAATTTGGTCAGATGCGTATG	1389
Db	313	ATCTGTACCTTGAATTCGAGCAGAACTCACCAAGCAATGGCAGAGATGAGAGAACTA	372	Qy	1393	TGATTTGGAGCAGTACAGCCAAATCAGAACTACTTCGGGCCCTGCAATGATGACACCATG	1452
Qy	376	ACCCGGGAAGAGGTCCAAACAGCCCAACAAACCAACCGCTCGACGCTCTGTTATAA	435	Db	1390	TGATTTGGGACAGCAACAGCCAAATCAGAACTACTTCCAAAGCCTGCAATGACCATATCATG	1449
Db	373	GGACTGGGAAGAAGGCGCTGAGCTTTAGACCAAGTCTTTGAAACCTCAATATATAA	432	Qy	1453	CCTACATGAACAAATTAATCTTAACTTGTGCAAAAAGCGAGTTCCGACTCTGGTATG	1512
Qy	436	ATGAGTATGCCGATGCCAGCTACACAACTGTGTGAAAAGATGCGTCAAAAGAACGCC	495	Db	1450	CCTACATGAACAAATTAATCTTAACTTGTGCAAAAAGCGAGTTCCGACTCTGGTATG	1509
Db	433	ATGAATTAATGATGCCACCTACACAACTAGTGGAAAGATGCGTGAAGGACTGCTC	492	Qy	1513	AAATATACATGGGACTCTCAAAGAAATGCTAGATGCTGATTTGCTTTAAGACCTTACCAA	1572
Qy	496	TCTACAGAAAGATTTGGTAGAGGAG---ATCTCTCTCACCGAGAGCCAGCCACAA	552	Db	1510	AAATATACATGGGAACTCAAAAGAAATCTAGATGAGTCCAACTTGTCTGAGAACTCCCGA	1569
Db	493	TCTACAGAAAGCAATTTGACAGAGAGAGAAATTTCCAGAGTGGAGCCAGCTCTCAGA	552	Qy	1573	CTACGGTCAGATTAGCCCTCGCCATTGATGTCGAACTTCCAGCATCATCAGCAAGTCGACT	1632
Qy	553	CTGCAAGCCACCGGCTGTACCCAGTAAAGAAAGCGATGATTAAGCCCAACAGAACATT	612	Db	1570	CAGCAATGAGTTGCTATTTGCCCTTGCATTAACCTTCAATATCATCGACAGTTGGAGT	1629
Db	553	CTGCAATGTCTACAAATATATCACCAAAACAGAGACAAATCCAAGCTAAAGACACC	612	Qy	1633	TGTTCAAGGGTTGTGATACACAGATGATTTATGACATGTTGCTTAAGATTTGAAATCCGTTTC	1692
Qy	613	ACTACAGGCTTTGTTGTTTCAAGTCAAAAGATGCTTTTAAACAGATCTTTAAAGCGAA	672	Db	1630	TATTCAGGGCTGTGACACACAGATGATTTATGACCTGCTGCTAAGATTTGAAATCCACTA	1689
Db	613	AAGACA---CGTTTCTTTTCAACCCAGAGAGTCCAGTAAAGAGACACCTACGAAGAA	669	Qy	1693	TCTATTTGCTCGTGACTTTGCTGCAAAAAGGGAGAAATTTGGCAAGGAAATGATATACA	1752
Qy	673	TTAAACTTCCAAACAGACATAGATTATACACAGATCGACTCTATCTCTGCTGGCTTTGC	732	Db	1690	TTTATTTACTGCTGGTACTTTGCTGCAAAAAGGGAGAAATTTGGAAGAAATGTCATACA	1749
Db	670	TGATCTTCCAGAGACATAGACTCTTACACAGATCGGGTCTATCTCTTGTGGCTCTGCTC	729	Qy	1753	TCAAGCATGGAGAAAGTCCAAAGTTCTTGGAGGCCCTGATGGTACTTAAAGTTCTGGTTACTC	1812
Qy	733	TTGTCACTTCTGCTTAACCTGGAACCTGCTGGTTTATACCACTGCGCTCGTCTTCCAT	792	Db	1750	TCAAAACAGGAGAGTCCCAAGTCTTGGAGGCCCTGATGGTCTCAAGTTCTTGGTTACTC	1809
Db	730	TTGTCACTTCTGCTTAACCTGGAACCTGCTGGTGTACCAAGTCCAGTGGCTCTGCTTCCAT	789	Qy	1813	TGAAGCTGGGTGCTGGTTTGGAGAAATCAGCCCTTCTAGCAGCAGAGAGAGAAACCGTC	1872
Qy	793	ATCAACCGGAGACAACTACTGCTGCTTATTCGGACATCATATGATATCATCT	852	Db	1810	TGAAGCTGGGTGCTGGTTTGGAGAAATCAGCCCTTCTAGCAGCAGAGAGAGAAACCGTC	1869
Db	790	GCCAAACACCAAGATAAAGAACTACTGGATTTATCTGACATCGTATGTGATCATCT	849	Qy	1873	GAACTGCCAATCTGTTGGGCCCCACGGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCC	1932
Qy	853	ACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGAGAGACATAA	912	Db	1870	GGACAGCTGATGTTGTGGCCCAAGGATTTGGCAATCTTTTAACTCTGACAAAAGAGCTC	1929
Db	850	ACCTTTGTGATATCTATTGATCCAGCCAGACTCCAAATTTGTAAGAGAGAGAGAAATTA	909	Qy	1933	TCCAAGAAATTTCTGTGCAATTTCAAACTTCTTAAAGCTCTCTCATGAAGAAAGCCAAA	1989
Qy	913	TAGTGGATTCMAATGAGCTAAGGAAACACTACAGGACTTCTCAAAATTTTCAAGTTGATG	972	Db	1933	TCCAAGAAATTTCTGTGCAATTTCAAACTTCTTAAAGCTCTCTCATGAAGAAAGCCAAA	1989
Db	910	TTGTAGATTCMAATGAGCTAAGGAAACACTACAGGACTTCTCAAAAGTTTTCGATGGATG	969	Qy	1993	TGCTTTTAAAGCAGAGGCTTAAGCCGAGAGACCCCTCCCAAGAAAGATCTTGGCC	2052
Qy	973	TGCGATCAATTAATACCAATTTGATATTTGCTACCTCTTCTTGGGTTTAAATCCCAATGTTA	1032	Db	1990	TTCTTTTAAAGCAGAGGAGGAAAGACCACTCAGGCAATCTCCTCAAGACAGGACCTGCT	2049
Db	970	TGGCATCTCTACTGCCATTCGAAGTTCTCTACATCTCTTTGGAGTTTAAATCCCATATCA	1029	Qy	2053	TGCTCTTCCACCGGAAAGAGAGACACCCAACTCTTTTAAACTCTCTCTAGGAGGACAG	2112
Qy	1033	GAGCAATAGAGATGTTAAAGTACACTCTTCTTAAATTTTGAATTTAATCATCACTAGAGCTA	1092	Db	2050	TTCTTTTCCCAACCAAAAGAGAGACACCCGGAATGCTTAAAGTCTCTCTAGGAAACACAG	2109

/protein_id="AAA5620.1"
/db_xref="GI:790511"
/translation="EPRELRIEPEKDEEEEEEEBEVTEVLDDSCVVSQVG
VQSEEDTRPOSTDQKLWEVGEAEKAEKAEAEVAAEAEKQPDMAETK
EPEPEAAEAASGVATKQHPQVEVDADSCPLMAENPPSTVLPPSPAKSDTK
VPSASGTHRKLLPDEDAEELKALSPAESFVWMSDPTPKDQDQRAASTASTN
SAIINDRLQELFKERTKVEKELIDPVTSDEESPKSPAKKAPAPDTPKPAEA
EVEBVEYCDMLCCCKHPKHPWKYPQPSIDPLTNLWVLMWLFVFWVAMNWCWLPK
RAAFYQTEPDTHHLLMDYLCOLYFLDITVQTRQFVGRGDIITDKKMNNLYK
SRFKMDLLSLPLDPLQKLVGVNPLLRPLRCLKYNMFAEENSRLSEILSKAVVRYI
RTAVYLLHNSCLYVWASAYQGLSHWYDVGNSYIRCYVPAVTKLTITGSLP
DKTLFEIVQLNFTGTVPASVMIGQNRDVVGAATQTYVRSCHDSTVKMMRYK
IPASQNRVKTWETVYHSGMDLSSELMVQPKRDLDAIDVNTNIVSKVAFPGC
DKQPMIDMLKRSVYVLPDVCYCKGEGIREMYIIQAGQVQLGPDGDKSVLVLTKA
GVSGFEISLLAYGGNNRNTNVAHFTNFIIDKKDLNEILVHYEPEKQLLRKLRRA
MURSNKPKBEKSVIILPPRAGTPKLFNAALMTKMGKGGKAGKGLAHLRAKLKLA
ALEAAKHEELVEYQAKSDQVGEESGAAPDQHTHEKAAOTPPAPRTPEPPGSPPS
SPPPASLGSCEGSEGPSEPEEHSVRICMSPPGPEQGLISLVKMPERESEKAR"

RESULT 6

1189	TGGACATACCGGTGTTCCAGACACGCTGCAGTTGTCAGAGCGGGGACATCATTTACGG	1241	Db
919	ATTCAAATGAGCTAAGGAACACTACAGGACTTCTACAAAATTTTCAGTTGGATGTCGCAT	978	QY
1249	ACAAAAGGACATGCGAAATACTACTCTGAAGTCTCGCGCTTCAAGATGGACCTGCTCA	1308	Db
979	CAATAATACATTGTGATATTTGCTACTCTCTCTTTCGGTTTTAATCAAATGTTTAGAGCAA	1038	QY
1309	GCCCTCGCGCTTGGATTTTCTATTGGAAGTGGTGTGAACCCGCTCCTCGCGCTGC	1368	Db
1039	ATAGGATGTTAAAGTACATTCATTTTTTTTGAATTTAAATCATCACTAGAGTCTATAATGG	1098	QY
1369	CCGCGTGTTTAAAGTACATCGGCTCTCTCGAGTTTAAACAGCCGCTTGAATCCATCTCTCA	1428	Db
1099	ACAAAGCATATATCTACAGAGTATTTCGAACAACTCGATACTTGTGTTTATTCTCGACA	1158	QY
1429	GCAAAGCCTACGTGTACAGGTTCATCAGAGCCAGCCTACCTTCTCTACAGCCCTGCATT	1488	Db
1159	TTAATGCCCTGTGTTTATTACTGGGCTTCAAATCATGAAGGAATGGCACCTACTAGATGGG	1218	QY
1489	TGAATTCCTGTCTTTATTACTGGGACTCGGCTATCAGGCGCTCGGCTCCACCTCACTGGG	1548	Db
1219	TGTTATGATGGGAAGAAACGAGTATCTCAGATGTTTATTATTGGGCAGITCGAACTTTAA	1278	QY
1549	TTTACGATCGGTGGGAACAGTTATTTTCGTGTTACTCTTTGCTGTGAAGACCCCTCA	1608	Db
1279	TTACCATGCGTGCCCTCCAGAACCAAACTTTATTGAAATTTGTTTTTCAACTCTTGA	1338	QY
1609	TCACCATCGGGGGCTGCGCTGACCCCAAGACACTCTTTGAAATTTGTTCTTCCAGCTGCTGA	1668	Db
1339	ATTTTTTTTCTGAGTTTTTGTGTTCTCCAGTTTAATTCGTTCAGATCAGAGATGTCATTG	1398	QY
1669	ATTATTTCACGGGCGCTTTTGTCTTCTGTGATGATCGGACAGATGAGAGATGTGGTAG	1728	Db
1399	GAGCAGCTACAGCCAAATCAGAACTACTTCGCGGCGCTGCATGGATGATGACACCAATTCCTTACA	1458	QY

QY	679	TTCAAACAGCATAGATTTCATAACAGATGCACTTATCTCTGTGGCTTGTGCTTGCTCA	738
DB	1988	TTCCCAGAGCAATTGACCCGCTCACCAACTGATGTATGTTCTTATGGCTGTTCTTCGTGG	2047
QY	739	CTCTTGGCTATACTGGACTGCTGTTTATACCACTGGCCCTCGTCTTCCCATAACAA	798
DB	2048	TGATGGCTCGGAATTGGAACGTGTGGCTGATCCCGTGGCTGGGCTTCCCCTACCAGA	2107
QY	799	CCGCAGACAATACACTACTGGCTTATTTCGGACATCATATGTGATATCATCTACTCTT	858
DB	2108	CCCGGACAATCCACCCTGGCTGCTGATGATTACCTATGCGACCTCATCTACTCTCC	2167
QY	859	ATGATATGCTATTATCCAGCCAGACTCCAGTTTGTAGAGAGGAGACATAATAGTGG	918
DB	2168	TGACATCATCCGTGTTCCAGACGCGTGCAGTTTGTTCAGAGCGGGGACATCATTCGG	2227
QY	919	ATTCAAATGAGCTAAGGAACAATACAGGACTTCTACAAATTTCAATTTGGATGTGCGAT	978
DB	2228	ACAAAGGACATGCGGAATAACTACTCGTAAGTCTCGCGCTTCAAGTGGACCTGCTCA	2287
QY	979	CAATAATACCATTTGATATTGTCTACTCTCTTCTTGGGTTTAATCCAAAGTTTAGAGCAA	1038
DB	2288	GCCTCTGCCCTTGGATTTTCTCTATTGAAGTCGGTGTGAACCCCTTCTCCGCGCTGC	2347
QY	1039	ATAGGATGTTAAAGTACACTTCATTTTTCGAATTTAATCATCACCTAGACTCATATAATGG	1098
DB	2348	CCGCTGTTTAAAGTACATGGCCCTTCTTCAGTTTAAACGCGCTGGATCCATCCTCA	2407
QY	1099	ACAAAGCATATATCTACAGAGTTATTTCGAACAACCTGGATACTTGTGTTTATTTCGACA	1158
DB	2408	GCAAAGCTACGTGTACAGGTCATCAGGACCCAGAGCTTACTTCTCTACAGCGCTGCATT	2467
QY	1159	TTAATGCCCTGTTTATTACTTGGGCTTCAAACATATGAAGAAATTTGGCACTACTAGATGGG	1218
DB	2468	TGAATTCCTGTCTTTATTCTGGCATCGGCTTACGGGCTTCGGCTCCACTCATCTGGG	2527
QY	1219	TGTATGATGGGAAGGAACAGATATCTGAGATGTTATTATTGGCAGTTTCGAACHTTAA	1278
DB	2528	TTTACGATGCGTGGGAACAGTATATTTCGCTGTTACTACTTTCGTGTGAAGACCTCA	2587
QY	1279	TTACCATTTGTTGGCTTCCGAAGACCACAACCTTATTTTGAATTTGTTTTCACTCTTGA	1338
DB	2588	TCACCATCGGGGGCTCGCTACCCCAAGACACTTTTGAATTTGCTTCCAGCTGCTGA	2647
QY	1339	ATTTTTTTTCTGAGATTTTTGTGTTCTCCAGTTTTAATTTGGTCAGATGAGAGATGTGATTG	1398
DB	2648	ATTATTTCAGGGGCTCTTTGCTTTCTCTGTGATGATCGACAGATGAGAGATGTGTTAG	2707
QY	1399	GAGCAGCTACAGCCAATCAGAACTACTTTCGGCGCTGCATGATGATGACCACTTGCCTACA	1458
DB	2708	GGGCGGCACCGGGGACAGACCTTACTACCGCAGCTGCATTTGAATTTGCTTCCAGCTGCTGA	2767
QY	1459	TGAACAATTTACTCCATTTCCTAACTTGTGCAAAAGCGAGTTTCGGACTTGTGATGAATATA	1518
DB	2768	TGAATTTCTACAGATCCCCAAGTCCGTGCAGAACCCGTCMAAGCCTGTCAGAGTACA	2827
QY	1519	CATGGGACTCTCAAAGAAATGCTAGATGATCTGATTTGCTTTAAGACCCCTACCAACTACGG	1578
DB	2828	CCTGGCACTCGCAAGGATGCTGTGATGAGTCAGAGCTGATGGTGCAGCTTCCAGACAAGA	2887
QY	1579	TCCAGTTAGCCCTCGCAATTGATGTGAACCTTCACATCATCAGCAAAAGTCGACTTGTTC	1638
DB	2888	TGCGGCTGGACCTCGCCATCGAGTGAACTTACACATCTGTTAGCAAAAGTCGACTCTTTC	2947
QY	1639	AGGTTGTGATPACACAGATGATTTATGACATGTTTGTCTAAGATTGAAATCCGTTCTCTATT	1698
DB	2948	AGGCTGTGACCGGCAGATGATCTTTGACATGCTTGAAGAGGCTTCGCTCTGTTGTCTTACC	3007
QY	1699	TGCTGTGTACTTTGTTCTGCAAAAGGAGAAATTTGGCAAGAAATGTATATCATCAAGC	1758
DB	3008	TGCCAAACGACTATGTGTGCAAGAGGGGAGATCGGCCGTGAGATGTACATCATCCAGG	3067
QY	1759	ATGAGAGAAGTCCAAAGTTCTTTGGAGGCCCTGATGTGTAATAAGTTCTCGTTACTCTGAAG	1818

Db		3068	CAGGGCAAGTGCAGGCTTTGGCGGCCCTCATGGGAATCTGTGCTGGTGACGCTGAAG	3127
QY		1819	CTGGGTCGGTGTGGAGAAATCAGCGCTTAGCAGCAGGAGGAGAAACCGTCGAAC	1878
Db		3128	CTGGATCTGTGTTGGAGAAATAAGCTTGTGCTGTGGGGCGGGAACCGGCGCACGG	3187
QY		1879	CCAAATGTGTGGCCACGGGTTGGCAATCTTTAATCTAGACAAGAACCCTCCAAG	1938
Db		3188	CCAACTGTGTGGCGACGGGTTTACCAACTCTTCATCTGGATTAAGAAGACCTGAATG	3247
QY		1939	AAATTCTAGTCGATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGTCTT	1998
Db		3248	AGATTGTGTGCTATCTCTGAGTCTCAGAGTTACTCCGAGAGAACCGAGCGCATGC	3307
QY		1999	TAAAGCAGAAGGCTAAGACCGCGAGAAG	2025
Db		3308	TGAAGACCAACAATAAGCCCAAGGAGG	3334

RESULT 8
AF042498

LOCUS Homo sapiens rod photoreceptor CNG-channel beta subunit (RCNC2)
mRNA, complete cds.

ACCESSION AF042498

VERSION GI:2921582

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4382)
Grunwald,M.E., Yu,W.P., Yu,H.H. and Yau,K.W.
Identification of a domain on the beta subunit of the rod
cGMP-gated cation channel that mediates inhibition by
calcium-calmodulin

JOURNAL J. Biol. Chem. (1998) In press

REFERENCE 2 (bases 1 to 4382)
Grunwald,M.E., Yu,W.P., Yu,H.H. and Yau,K.W.
Direct Submission
Submitted (12-JAN-1998) Neuroscience, Johns Hopkins University
School of Medicine, 725 N. Wolfe St., Baltimore, MD 21205, USA

FEATURES source

- 1..4382 Location/Qualifiers
- /organism="Homo sapiens"
- /mol_type="mRNA"
- /db_xref="taxon:9606"
- 1..4382 /gene="RCNC2"
- 71..3808 /gene="RCNC2"
- /note="cyclic nucleotide-gated cation channel beta subunit"
- /codon_start=1
- /product="rod photoreceptor CNG-channel beta subunit"
- /protein_id="AAC04830.1"
- /db_xref="GI:2921583"
- /translation="MLGWQRVLPPQPGTRPKTKMQEEVEPEPEMAEAVEBPENPNE
EATESSPMPESFKEEVAVADPSQETKEALTSTISLRQAQAISENKSPSHRLL
LTLMKGVEKVIPOPHVSIITEDPAIILGHSTGDTGDFEALAEAQDTPGLRLLE
WLEONLBRVLPPQPKSEVRDEPAVAPPGRQEMGPKLQARETSLPTPIPLQAP
EEKPAEPQPKSQACTSSLPTRDPARLVWLHLRLEMALPOPVLHGIGIQEPEPL
SPGICDVQTISIPLGGQVEDPLVLEEVPWEADHDQVTSQCQTVVPAVEENKA
KMPELRURIIEEKEDBEHEEBEEEEVEEIVLDSCVSVGVQSSEDGTCPQ
STDQLUWEVEEGEAKEAKEABEVAEEAEKEPDQNAETKEEPRAEBAASAS
GVATKOPQVQVEDTDADSCPLMAENPFSTVLPPPSPAKSDTLIPVSSASGTHRK
LPSEDDBAELKALSPEAVMSDPTTKTDQDGRAASTNSAIINDRILOEQL
KLPERTEKVKEKLIKIDPVTSDESPKSPAKPAEPAPTCKAEAPVEEHYCDML
CCFKPRKPWKVKQPQOSIDPLTNLMVYLFPVVMAWNMNCKLIKPSWAPEPYQPDNI
HWLLMDXLDLYFLDIITWFQTELQFVRGDIIITDKKWENNVLKSRFRKMDLLSH
PLDFLYLKGNVPLLRLPCRLKYMAPFEFNRSLSILSKAYVSIVRTAYTVALYSLIH
NSCLYYWASAYGSHRWVGNSIRCIYFAVKLIITILSGLDPKTFEIFVQ

LNYFTGVFAFSVMIGQMDVUGAATAGATYVRSCHDSTVKYMNFKYKPKSVQNVKWTW
 XYETHSOMGLDESELMVOLDPKRDLDAIDVNNYINVKVALFGCDRQMIKFNKRL
 RSVYLPNDYVCKGEIGREMYITQAGQVVLGPDGKSVLTVLKAGSVFGEISLLAV
 GGNRRTANVAHGFTNLFILDKKDLNEILVHPESQKLRKRLKRLMLRNNKPKKEK
 SVLILPPRAGTPKLNFALAMTGMKGKGLAHURLKRLKRLALEAAKQOELV
 BOAKSSQDVKEEGSAPDQHTHPKEATDPAPRTPEPPGSPSPSPPPASLGRPEG
 BEEGPAEPEHSVRICMSPGPEPQILSVKMPERBEKAE"

ORIGIN

Query Match 21.4%; Score 577.4; DB 9; Length 4382;
 Best Local Similarity 64.3%; Pred. No. 8.4e-101;
 Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

QY	679	TTCCAAACAGCATAGATTATACACAGATCGACTATCTCTGCTGGCTTGGCTTGTCA	738
Db	1983	TTCCCCAGAGCATGACCGCTGACCAACCTGATGATGCTCTATGGCTGTTCTTCGTGG	2042
QY	739	CTCTTGGCTTAACTGGAACTGCTGGTTTATACCACCTGCGCTGCTTCCCATATCAAA	798
Db	2043	TGATGGCTTGAATTGGAACCTGTTGGCTGATTCCCGTGGCTTCCCTACCAGA	2102
QY	799	CGCAGACAAATACACTGCTGCTTATGCGGACATCATATGATGATCATCTACCTTT	858
Db	2103	CCCCGGAACAATCCACACTGGCTGCTGATGGATTACCTATGCGAATCATCTACTTCC	2162
QY	859	ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTG	918
Db	2163	TGGACATCAGCGTGTTCAGACAGCGCTGAGTTTGTTCAGAGGGGGGACATCATACGG	2222
QY	919	ATTCAATAGAGTAAGGAAAACACTACAGACTTCTPACAAAATTTGAGTTGGATGTCGAT	978
Db	2223	ACAAAAGGACATCGAAATAACTACTCTGAAGTCTCGCGCTTCAAGATGAGACCTGTCTCA	2282
QY	979	CAATAATACCATTTGCATATTTGCTACCTCTCTTTGGTTTAAATCAATGTTTAGACAA	1038
Db	2283	GCCTCTCGCTTGGATTTTCTTATTTGAAAGTCGGTGTGAAACCCCTCTCCGCTGC	2342
QY	1039	ATAGATGTTAAAGTACACTTTTATTTTGAATTAATCATCACTAGAGTCTATAATGG	1098
Db	2343	CCCGCTGTTTAAAGTACATGCGCTTCTTCGAGTTTAAACAGCGCTGGAATCCATCTCA	2402
QY	1099	ACAAGCATATATCTACAGAGTATTGCAACCTGGATCTGCTGTTTATTTCTGCACA	1158
Db	2403	GCAAGCCTACGTGACAGGTCTACAGACCAAGCTACCTTCTCTACAGCCTGCTATT	2462
QY	1159	TTAATGCTGCTTATTTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG	1218
Db	2463	TGAATCTGCTTATTTACTGGGCTGCTATCAGGCTCGCTCCACTCAGTGG	2522
QY	1219	TGTATGATGGGAGGAAACAGATCTGAGATGTTTATTTGGGAGTTCGAACTTTAA	1278
Db	2523	TTTACGATGGGCTGGGAAACAGTATATATTCGCTGTTACTTCTGCTGTGAAGACCTCA	2582
QY	1279	TTACCATGTTGGCTTCCGAAACACAACTTTTATTTGAAATTTTCAACTCTTGA	1338
Db	2583	TCACCATGGGGGCTGCTGACCCCAAGACACTTTTGAATTTGCTTCCAGTCTGA	2642
QY	1339	ATTTTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1398
Db	2643	ATTATTTTCCAGGGGCTTCTGCTTCTGATGATCGGACAGATGAGAGATGTTGGTAG	2702
QY	1399	GAGCAGCTACAGCAATACAGAACTTCTCCGCGCTCATGGATGACACCATTCCTTACA	1458
Db	2703	GGGCGGACCGGGGACAGACTTCTACCGAGCTGATGACAGCAGCGTGAAGTACA	2762
QY	1459	TGAACAATTTACTTCAATTTCTTAACTTTGCAAAAGCGAGTTCGAGTTCGATCAATATA	1518
Db	2763	TGAATTTTCAAGATCCCCAAGTCCGTGCAAGACCGCTCAAGACCTGGTACGAGTACA	2822
QY	1519	CATGGACTCTCAAGATGCTAGATGCTGATTTGCTTGAACCTTACCACTACGACG	1578
Db	2823	CCTGGCACTCGAAGGATGCTGGATGAGTCAAGCTGATGGTTCAGCTTCCAGACAAGA	2882

QY	1579	TCAGTTAGCCCTCGCCATTGATGTAACCTTACAGCATATCAGCAAAAGTCGACTTGTCA	1638
Db	2883	TGGCGTGGACCTCGCCATCGACGTGAATACAAATCGTTAGCAAGTCGCACTTTTC	2942
QY	1639	AGGTTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTTATT	1698
Db	2943	AGGCTGTGACCGGAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTTGCTTACC	3002
QY	1699	TGCTCTGCTACTTGTCTGCAAAAAGGAGAAATTTGGCAAGCAAAATGATATCATCAAGC	1758
Db	3003	TGCCCAACCACTATGTTGCAAGAAAGGGGAGATCGGCGTGATGATCATCATCCAGG	3062
QY	1759	ATGGAAGTCCAAAGTTCTTGGAGCCCTGATGCTACTTAAAGTTCTGTTACTCTGAAAG	1818
Db	3063	CAGGCAAGTGCAGGCTTGGGGCGGCTTGAAGGAAATCTGCTGTTGAGCTGAAAG	3122
QY	1819	CTGGTCTGCTGTTTGGAGAAATCAGCTTCTAGCAGGAGGAGGAGAAACCGTTCGAACTG	1878
Db	3123	CTGATCTGTTTGGAGAAATAAGCTTCTGCTGCTTGGGGCGGGAACCGGCGCACGG	3182
QY	1879	CCATGCTGCTGCGCCACGGTTTGGCAATCTTTAACTCTAGACAAAAGACCTCCAG	1938
Db	3183	CCAACTGCTGCGGACGGTTTACCAACCTTCTCATCTGATGAAGAGGACCTGAATG	3242
QY	1939	AAATTTCTAGTATTCAGATTCAGAAATCTGTAAGGATCTCATGAAGAAAGCCAGAGTCTTT	1998
Db	3243	AGATTTTGTGCTATCTGATCTCAGAGTTACTCGGAAGAAAGCCAGGCGCATGC	3302
QY	1999	TAAAGCAGAGGCTTAAGCCGAGAG 2025	
Db	3303	TGAGAGCAACAATAAGCCCAAGGAGG 3329	

BC045114 4763 bp mRNA linear ROD 16-SEP-2003
 Mus musculus cyclic nucleotide-gated channel beta subunit 1, mRNA
 (cDNA clone IMAGE:4504353), partial cds.
 BC045114
 BC045114.1 GI:28175674

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 4763)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.X., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahy, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y., Krzywicki, M.I., Skalska, U., Smallos, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 2338257
 PUBMED
 12477932
 2 (bases 1 to 4763)
 Strausberg, R.
 Direct Submission
 Submitted (27-JAN-2003) National Institutes of Health, Mammalian

TITLE
 JOURNAL
 MEDLINE
 2338257
 PUBMED
 12477932
 2 (bases 1 to 4763)
 Strausberg, R.
 Direct Submission
 Submitted (27-JAN-2003) National Institutes of Health, Mammalian

1219 TGATGATGGGAGGAAACGAGTATCTGAGATGTTATTATTGGGAGTTCGAACCTTAA 1278
1486 TTTATGATGGCGGGAACAGATTACCTGCTGTTACTACTGGCTGGAAGACCCCTCA 1545
1279 TTACCAATGGTGGCTTCCAGAACCAACAACTTTATTTGAAATGTTTTCACACTTTGA 1338
1546 TCACCAATGGCGGCTGCCCGAGCCCGAGGACGCTCTTTGAAATGTTTTCAGGCTCAA 1605
1339 ATTTTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1398
1606 ACTATTTCCAGGGCGTCTTCCGCTTCTCGTGAATCGAAGAGAGAGAGAGAGAGAGAG 1665
1399 GAGCACTACAGCAATCAGAACTACTTCCGGGCTGATGATGATGATGATGATGATGATGAT 1458
1666 GGCGCCGACCGGGGACAGACTACTACCGCAGCTGATGATGATGATGATGATGATGATGAT 1725
1459 TGAACATTAATCTCCATCTTAACTTGTGCAAAAGGAGTTCGGACTTGGTATGATGATGAT 1518
1726 TGAATTTTACAGATGATCCCGAGTCCGTCAGACACCGGCTCAAGACCTGGTACGAATACA 1785
1519 CATGGGACTCTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGATG 1578
1786 CTGGGACTCTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGATG 1845
1579 TCAGTTAGCTTCCGCTTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATG 1638
1846 TCGGCTGAGCTTCCGCTTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATG 1905
1639 AGGGTGTGATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1698
1906 AGGGTGTGATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1965
1699 TCCTGTGATCTTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGATG 1758
1966 TGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2025
1759 ATGAGAGAGTCAAGTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGATG 1818
2026 CGGGCAGTGCAGGCTCTGGTGGCCCGGATGATGATGATGATGATGATGATGATGATGATG 2085
1819 CTGGTCTGGTGTGGAGAAATCAGCTTCTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1878
2086 CTGGATCTGTGTCGAGAAATAGCTTGTGCTGATGATGATGATGATGATGATGATGATGATG 2145
1879 CCAATGTGTCGTCGAG 1938
2146 CTAAGCTGTGTCGAG 2205
1939 AAATTTCTAGTCAATATCCAGATCTGAAAGGATCTCATGAGAGAGAGAGAGAGAGAGAG 1998
2206 AAATTTCTAGTCAATATCCAGATCTGAAAGGATCTCATGAGAGAGAGAGAGAGAGAGAG 2265
1999 TAAAGCAG 2023
2266 TGAGAAATTAACAAG 2290

RESULT 12
LOCUS BTNG4CGN
DEFINITION B.taurus mRNA for CNG4c protein.
ACCESSION X94707
VERSION X94707.1 GI:1154636
KEYWORDS CNG4c gene; CNG4c protein; cyclic nucleotide-gated cation channel; modulatory subunit.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1
AUTHORS Biel.M., Zong.X., Ludwig.A., Sautter.A. and Hofmann.F.
TITLE Molecular cloning and expression of the Modulatory subunit of the

cyclic nucleotide-gated cation channel
J. Biol. Chem. 271 (11), 6349-6355 (1996)
96198098
8626431
2 (bases 1 to 3253)
Biel.M.
Direct Submission
Submitted (08-JAN-1996) M. Biel, Inst. f. Pharmakologie und
Toxikologie, Technische Universität München, 80802 München,
Biedersteiner Strasse 29, FRG
Location/Qualifiers
1. 3253
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="testis"
/clone_lib="cDNA in plasmid vector pCDNAII (Invitrogen)"
/dev_stage="adult"
1. 3253
/gene="CNG4c"
55..2874
/genes="CNG4c"
/note="modulatory subunit of cyclic nucleotide-gated
cation channel"
/codon_start=1
/product="CNG4c protein"
/protein_id="CAA64367.1"
/db_xref="GI:1154637"
/db_xref="GOA:Q28181"
/translation="MRAGQKGRCHSVLLDYLVSQSEEDQSEBETQDQSEVGGAAQ
GVGGAQALSESESTQDQSEVGGAAQSEVGGAAQSEVGGAAQSEVGGAAQSEVGGAAQSEVGGAAQ
VQSEALADSSGVPATPEHPELOVEDADSRPLIASENPPSVQLSPAKSDTLA
PQSGATGSLRKLPSQDDEBELKMLSPAAPSVAVMSPTSPQGTDDOATSTASQ
SAINDRQELVKLFKTEKVKELIDPVTDESPSPAKAPAPAPAPAPAPAPAPAPAPAPAPAPAP
GOVEEHCEMLCCFKRPPKWKYQFPOSIDPLTNLYLWLFVFLVLANWNCWLPV
RWAFYQPTDNLHLWLDLYLDLITVQMLQFVRGGDITDKKEMNNYVR
RTTAYLLSLHLNSCLYVWAGELGTHWYDVGNSYIRCYWAVKTLITIGGLP
DPTFLVFOGLNYFTGVFAFVIMGOMRVGAATAGATVYSCDSTVYKMFYK
IPRSQNVKTKWYETWHSQKMLDESELVQLPKMLDLALDLYNYSIVSKVALFOGC
DRQMLFKLRSLVYLNDIVCKGEIGREMYIIQAGQVVGSGDGKSLVLTAKA
GVGFEISLLAVGGNRRATNVVAHGFNLFLDKDLNLEILVHYSPQKLRKARR
MLRNNKPKESVILIPRAGTPKLFNAALAAAGKMGAGKGGRLALLRLKELAA
LEAARQQQLLEQAKSDEDAVGEESAAPEQPPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP
PAPAPAPSPPPASQPERPEDGKAAARPEEHVIRHVTLPDPSPSEQLLVVEVPEKOE
EKEKEETEEKEEKEEKEEKEE"
229..282
/gene="CNG4c"
/note="deletion present in CNG4e variant"
249..275
/gene="CNG4c"
/note="deletion present in CNG4d variant"
misc_feature
misc_feature
ORIGIN
Query Match 21.2%; Score 572.2; DB 4; Length 3253;
Best Local Similarity 64.1%; Pred. No. 8.6e-100;
Matches 862; Conservative 0; Mismatches 483; Indels 0; Gaps 0;
QY 679 TTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTCTGGCTCTGCTTGTGCA 738
Db 959 TTCCCCAGAGCATGACCCGCTGACCACTGATGATGATGATGATGATGATGATGATGATG 738
QY 739 CTCCTGCTTAATGAGACTGCTGGTGTATACACCTGGCGCTCGTCTTCCATATCAAA 798
Db 1019 TGCTGGCCTGAACTGGAACCTGCTGGTGTATCCCGCTGGCGCTTCCCTATCAGA 1078
QY 799 CCGCAGACAAATACACTACTGCTGCTTATTTGGGACATCATATGATATGATATCTACCTTT 858
Db 1079 CGCCAGACAAATCCACTCTGGCTGCTGATGATGATGATGATGATGATGATGATGATG 1138
QY 859 ATGATATGCTATTATTCAGCCCAAGATCCAGTTTGTAAAGAGAGAGAGATATAGTGG 918

Db	1139	TGACATACCGTGTCCAGATCGCTGCGTTCAGTTCGTGACAGCGGGACATCATTTACGG	1198
Qy	919	ATTCAATAGACCTAAGAAACACTACAGACTTCTACAAATTTTCAGTTGGATGTCGAT	978
Db	1199	ACAAAAGGAGATGCGCAAAATACGTGAATCTAGCGCTTTAAGATGACATGCTCT	1258
Qy	979	CAATAATACCATTTGATTTTGTCTTCTCTTGGTTTAACTCAATGTTTAGAGCAA	1038
Db	1259	GCCTCTTGGCTTGGACTTACTCTACTTGAATTCGCTGTAATCCCTCTCGCTTGC	1318
Qy	1039	ATAGATGTTAAGTACACTTCAATTTTGAATTAATCATCATCAGTACAGTCTAATAGG	1098
Db	1319	CCGCTCTTGAAGTATATGCTCTTCTTGGTTTAAACACCGCTGGAATCCATCTCA	1378
Qy	1099	ACAAAGCATATATCTACAGAGTTATTCGAAACACTGATCTTCTGCTTTATCTGACA	1158
Db	1379	GCAAGCTAGTTTACAGGGTATACAGACCACTACCTACTCTCTACAGCTTACATC	1438
Qy	1159	TTAATGCTGTGTTTATCTGGCTTCAAACTAAGAAATGGCACTACTAGATGGG	1218
Db	1439	TGAATCATGCTCTTATTAATCTGGCATCGGCTATGAGGCTCGGCTCCACTCACTGG	1498
Qy	1219	TGATATGCGGAGGAAAGAGTATCTGAGATCTTATTTATGGCAGTTTCAACTTAA	1278
Db	1499	TTTATGATGGCTGGGAAACAGTTACATTCGCTGTTACTTCTGCTGTGAAGACCTCA	1558
Qy	1279	TTACCATTTGCTGCTTCCAGAACCAAACTTTATTTGAATTTGTTTCAACTCTGA	1338
Db	1559	TCACCATCGGCGCTGCCGACCCAGGACGCTCTTTGAAATTTGCTTCCAGGCTTAA	1618
Qy	1339	ATTTTCTTTTCHGAGTCTTTTGTCTTCCAGTTTAAATGTCAGATCAGAGATGATG	1398
Db	1619	ACTATTTTACGGGCTCTTCTGCTTCTCCGATGATCGGACATGAGAGATAGTGG	1678
Qy	1399	GAGCAGCTACAGCAATCAGAACTACTTCCGCGCTCATGATGATGACACCACTTCC	1458
Db	1679	CGGCGCACCGCGGACAGACCTTACTACCGACCTGCAATGACAGACCGTGAAGTAT	1738
Qy	1459	TGAACAAATTAATCCATCTTAAATTTGTGCAAAAGCGAGTTCCGACTTGGTATGAAT	1518
Db	1739	TGAATCTTCAAGATCCCAAGTCCGTCGAGAACCGGCTCAAGACCTTGTACGAATACA	1798
Qy	1519	CATGGACTCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG	1578
Db	1799	CCTGCACTCCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG	1858
Qy	1579	TCCAGTTAGCCCTCGCCATTTGATGTGAATTTGACATCATCAGCAAAAGTGTGTC	1638
Db	1859	TCCGCTGACCTCGCCATTTGACGTGAATTTTCCATCGTCAGCAAAAGTGTGTC	1918
Qy	1639	AGGTTGTATACACAGATGATTTATGATGATGATGATGATGATGATGATGATGATG	1698
Db	1919	AGGCTGTGACCGGCAGATGATCTTTGATGATGATGATGATGATGATGATGATGATG	1978
Qy	1699	TGCTGTGTGACTTTCTGCAAAAGGAGAAATTTGCAAGAAATGTATATCATCAAGC	1758
Db	1979	TGCCAATGATTAATGCTGTGCAAGAGGGGAGATAGCGCGGAAATGTATCATCAGG	2038
Qy	1759	ATGAGAGATCCAAATTTGAGGCGCTGATGATGATGATGATGATGATGATGATGATG	1818
Db	2039	CGGGCAGGTGACGCTTCTGCGTGGCGGATGCGAAATCCCTGCTGCTGCTGCTG	2098
Qy	1819	CTGGGTGCTGTTTGGAGAAATCACTCTTCTAGCAGAGGAGGAGAAACCGTCAAGCT	1878
Db	2099	CTGGATCTGTTTTCGAGAAATTAAGCTTCTGCTGTTAGGGCGGGACCGCGCACAG	2158
Qy	1879	CCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1938
Db	2159	CTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2218
Qy	1939	AAATTTCTAGTCAATTAATCCAGATCTGATGATGATGATGATGATGATGATGATG	1998
Db	2219	AAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2278

1999	TAAAGCAGAGGCTAAGACCGCAGA	2023			
2279	TGAGAAATACACAGGCCCAAGGA	2303			
RESULT 13	AF074014	3290 bp	mRNA	linear	MAM 30-OCT-2001
LOCUS	Bos taurus cyclic nucleotide-gated channel beta subunit 1e				
DEFINITION	(CNCbeta) mRNA, complete cds.				
ACCESSION	AF074014				
VERSION	AF074014.1	GI:3309625			
KEYWORDS	Bos taurus (cow)				
SOURCE	Bos taurus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 3290)				
AUTHORS	Wiesner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and Weyand, I.				
TITLE	Cyclic nucleotide-gated channels on the flagellum control Ca2+ entry into sperm				
JOURNAL	J. Cell Biol. 142 (2), 473-484 (1998)				
MEDLINE	98345361				
PUBMED	9679145				
REFERENCE	2 (bases 1 to 3290)				
AUTHORS	Wiesner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and Weyand, I.				
TITLE	Direct Submission				
JOURNAL	Submitted (24-JUN-1998) IBI, FZ-Juelich, Leo-Brandt-Strasse, Juelich, NRW 52425, Germany				
FEATURES	Location/Qualifiers				
source	1..3290				
gene	/organism="Bos taurus"				
CDS	/mol_type="mRNA"				
	/db_xref="taxon:9913"				
	1..3290				
	/gene="CNCbeta"				
	200..3058				
	/codon_start=1				
	/product="cyclic nucleotide-gated channel beta subunit 1e"				
	/protein_id="AAC26129.1"				
	/db_xref="GI:3309626"				
	/translation="MNVIAPLSCTIMASLIATKAPNHSLVLDLSVLVPOSEEDRSES ETDQSEVGAQAQGEVGAQAALSESETQDQSEVGAQAQDQSEVGAQAQGEVGAQAQ QDQVGAQAQDQSTHQLQEEALADSSGVPAEHEPQLQVEDADSRPLAENPSP VPLPSAKSDTLAVGSATSLKRLKSPQDDEELKMLSPAAPVVAWSPTSPQG TDQDRATSTAGNSAIINDRLQELVKLFKERTKEKLIIDPVTSEESPKSPAK KAPEPAPEVKAEGQVEBEHYCEMLCKKRRPKKYQFQSIDPLTLMILWLF VVLAWNWCNLIPIVWAFYQPDNIHLWLLDYLCDLILYLDITVQMLQFVRGGD IITDKEMNNIVKSORFKMDMLCLLPDLLVLEKGVNPLLPCLKYMFEFNNR LSILSKAVYRVIRTTATLLYLSHLNLSCLYTWASAYEGLSGTHWYDVGNSYIRCY YNAKTLITIGLDPDPTLFIQVGLNYFTGVFAFVSMIGNRDVVGAATAGQTYR SCMDSTVKNFYKI PRSQNRVKTWYTHSQGLMDESLMVLPDMRLDLA:DV NTSIVSKVALFOCDRCQYFDMLKRLSVYLPNDYVCKKGEIGREMYIIQAGQVQL GGDGKSVLTKAGSVFGEISLLAVGGNRRNTANVAVGFTNLFLDKKDLNEILVH YPSOKLLEKARMLRNKKPKESVLILPPRAGTPKLPAALAAAGKMGAKGSGG RLALLARLKLALAAARQQQLLEQAKSDEDAVGEESASPEOPPRPEPPAPAP APPTAPEPLAPEAPAPAPSPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP EQILLVEVPEKQBEKEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE				
ORIGIN					
Query Match	21.2%;	Score 572.2;	DB 4;	Length 3290;	
Best Local Similarity	64.1%;	Pred. No. 8.6e-100;			
Matches	862;	Conservative	0;	Mismatches 483;	Indels 0; Gaps 0;
Qy	679	TTCCAAACAGCATAGATTATACACAGATGACATCTATCTCTGTGGCTCTTCTGTGCA	738		
Db	1146	TTCCCAAGCATCGACCCGCTGACCAACCTGATGATACATCTTGTGCTTCTTCTGTGG	1205		

VFOGLNYFTGVFAFPAFVWIGCMRDVVGAAATAGOTVYRSOMDSTVKYMFVKLPSVQNR
VKTWYTVHWSQMLDESIMVQLPDKMRDLDAIDVNSIVSKVALPQCCBROMFIDM
LKLRSVYLPNDYVCKGEIGREMIYIIQAGVQVLLGGDDSKSVLITLKAGSVFGEIS
LLAVGGNRTANVAVHFTNFIIDKOLNEILHYPPESQMLKLRKGRARMLRNKKP
KEKSVILIPRAGTPKLFNAALAAAGKMGKGRGRLLARLKEALAAALRNKKQ
OLLEOASSEDAVVEGSGASPEOPRPPPPAPAPAPPTAPPEPLAPPEAPAPAP
SSPPPASQSRPEGDKDAARPEHPVRIHVLPDPSEQILLVVEPKEKEKEEET
BEKESEBARKEKEE

ORIGIN		Query Match	21.2%; Score 572.2; DB 4; Length 4282;
		Best Local Similarity	64.1%; Pred. No. 8.4e-100;
		Matches	862; Conservative 0; Mismatches 483; Indels 0; Gaps 0;
Qy	679	TTCCAAACACATAGATTATACACAGATCGACTCTATCCCTGTGCTCTTCTGTCTCA	738
Db	2315	TTCCCAAGACATGACCCGCTGACCAACCTGATGATACATCTTTGTGGCTGTTCTTCTGG	2374
Qy	739	CTTTGGCTATAACTGGAATGCTGTTTATACCACTGCGCCTCGTCTTCCCATATCAAA	798
Db	2375	TGCTGGCTGGAATGAACTGCTGGCTGATTCCTGGTGGCTTCCCTCATCAGA	2434
Qy	799	CCGAGACACATACACTACTGGCTTATTCGGACATCATATGTGATATCATCTTCTT	858
Db	2435	CGCCAGACAACTCCACTCTGGCTGCTGATGATTACCTGTGTGACCTCATCTACTCTC	2494
Qy	859	ATGATATGCTATTATCCAGCCAGACTCCAGTTTGTAGAGGAGGAGACATATAGTGG	918
Db	2495	TGGACATACCGTGTTCCAGTGGCCTCGAGTTTGTACAGGCGGGACATCATTAAGG	2554
Qy	919	ATTCAAAATGAGCTAAGAAACACTACAGACTTCTCAAAATTTAGTTGGATGTGCGAT	978
Db	2555	ACAAAAGGAGATCGGCAACAAATTAAGTAAATCTCAGCGCTTTAAGATGGACATGCTCT	2614
Qy	979	CAATAATACCATTTGATTTGCTACCTCTTCTTGGGTTTAACTCCAACTTTTAGAGCA	1038
Db	2615	GCCTCTTGGCCTTGGACTTACTCTACTTGAAATTCGGTGTGAATCCCTCGCGCTGC	2674
Qy	1039	ATAGGATGTTAAAGTACACTTCATTTTGAATTTAATCATCATCACTAGACTCTATAATGG	1098
Db	2675	CCGCTGTTTGAAGTATATGCGCTCTTGTAGTTTAAACCGCTCGAATCCATCTCA	2734
Qy	1099	ACAAAGCATATCTACAGAGTTATTCGAACACTGATGACTTCTGCTTTTATCTGCACA	1158
Db	2735	GCAAGGCTACGTTTACAGGTTTATCAGGACCAAGCTTACCTGCTCTACAGCTTACATC	2794
Qy	1159	TTAATGCTGTGTTTATTACTGGCTTCACAACTATGAAGAAATGGCACTACTAGATGGG	1218
Db	2795	TGAATCATGTCTTATTACTGGCATCGGCTATGAGGCTCGGCTCCACTCACTGGG	2854
Qy	1219	TGTATGATGGGGAAGGAAACAGATATCTGATGTTTATTATTTGGGCACTTGAACCTTAA	1278
Db	2855	TTTATGATGGGCTGGGAAACAGTTACATTCGCTGTTACTTCTGCTGTGAAGACCTCA	2914
Qy	1279	TTACCATGTTGGCTTCCAGAACCAAACTTTTGAATTTGAAATTTTCAACTCTTGA	1338
Db	2915	TCACATCGGGGCTGCGCACCCAGGACGCTCTTTGAATTTGTTTCTCAGGCTTAA	2974
Qy	1339	ATTTTCTTCTGGAGTTTCTGTTCTCCAGTTTAAATGTTGTCAGATGAGATGTGATG	1398
Db	2975	ACTATTTTCAAGGCTCTTCTGCTTCTTCTCGTGATGATCGGACAGATGAGACGTAGTGG	3034
Qy	1399	GAGACGTACAGCCATCAGAACTACTTCCCGGCTGCGATGATGATGACACCTTCCCTACA	1458
Db	3035	GGGCGCCACCGGGACAGACCTTACTACCCAGCTGATGGACAGCACCGCTGAGTATA	3094
Qy	1459	TGAACAAATTTCTCAATCTTCAACTGTTGCAAAAGCGAGTTTCGACTTGGTATGAATATA	1518
Db	3095	TGAATCTTCAAGATCCCGAGTCCGTTGAGAACCGGCTCAAGACCTGGTACGAATACA	3154
Qy	1519	CATGGACTTCAAGAATGCTAGATGATGCTGATTTGCTTAAAGACCTTCAACACTACGG	1578
Db	3155	CCTGGCACTCCCAAGGATGTTGGATGATGATGATGATGATGATGATGATGATGATGATG	3214

Qy	1579	TCCAGTTAGCCCTCGCCATTTGATGTGAACCTTACGATCATCATCAGCAAAAGTCGACTTGTTC	1638
Db	3215	TGGGCTGGAACCTGCCCATTGACGTGACTTATTCATCTGTCGAGCAAAAGTGGCACTCTTCC	3274
Qy	1639	AGGTTTGTATACACAGATGATTATGACATGTTGCTTAAGATTGAAATCCGTTCTCTATT	1698
Db	3275	AGGCTGTGACCGGCGAGATGATCTTTGACATGCTCAAGAGGCTCGGCTCTGTAGTCTTACC	3334
Qy	1699	TGCTGTGTGACTTTGCTGCAAAAGGAGAGAAATGGCAAGAAATGTATATCATCAAGC	1758
Db	3335	TGCCCCAATGATTACGTGTGCAAGAGGGGAGATAGCCCGGGAATGTACATCATCCAGG	3394
Qy	1759	ATGAGAAAGTCAAGTCTTCTGGAGCCCTGATGTACTTAAAGTTCTGGTTACTCTGAAAG	1818
Db	3395	CGGGCACGTGCAGTCTTGGTGGCCGATGGAATCGTGTGCTGACGCTGAAGG	3454
Qy	1819	CTGGTCTGGTGTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTGAACCTG	1878
Db	3455	CTGGATCTGTGTTCGAGAAATAAGCTTCTGGCTGTAGGGGGCGGGAACCGGCCACAG	3514
Qy	1879	CCAAATGTGTGGCCCAACGGTTTGGCAATCTTTAACTCTAGACAAAGAACCTTCCAAAG	1938
Db	3515	CTAACGTGTGGCCCATGGTTTACCAACCTCTTCTGATTAAGAGGACCTGAATG	3574
Qy	1939	AAATTTAGTGAATTCACGATTCGAAAGATCTCATGAAGAACCCAGAGTGTCTT	1998
Db	3575	AAATTTCTGTGATTCATTCGAGTCTCAGAAAGTTGCTCCGCAAGAACCCAGGAGATGC	3634
Qy	1999	TAAGCAGAGGCTTAAGACCGCAGA	2023
Db	3635	TGAGAAATTAACAAGCCCAAGGA	3659

RESULT 15
RNCNG41
LOCUS
DEFINITION
Rattus norvegicus mRNA for cyclic nucleotide-gated cation channel
beta subunit.
ACCESSION
AJ000496
VERSION
AJ000496.1 GI:2292985
KEYWORDS
beta subunit; CNG4.1 gene; cyclic nucleotide-gated cation channel.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1
AUTHORS
Sautter, A., Biel, M. and Hofmann, F.
TITLE
Molecular cloning of cyclic nucleotide-gated cation channel
subunits from pineal gland
JOURNAL
Mol. Brain Res. 47, 171-175 (1997)
REFERENCE
AUTHORS
Sautter, A.
TITLE
Direct Submission
JOURNAL
Submitted (17-JUL-1997) Sautter A., Institut f. Pharmakologie u.
Toxikologie, Technische Universitaet Muenchen, Biedersteiner Str.
29, D-80802 Muenchen, GERMANY

FEATURES
source
1. .4238
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
gene
1. .4238
/genes="CNG4.1"
59. .4078
/genes="CNG4.1"
/codon_start=1
/product="cyclic nucleotide-gated channel beta subunit"
/protein_id="CAA04133.1"
/db_xref="GI:2292986"
/db_xref="GOA:O35788"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 17:15:00 ; Search time 1007.37 Seconds
(without alignments)
11398.850 Million cell updates/sec

Title: US-09-855-828-2
Perfect score: 2703
Sequence: 1 catttctacctaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002s.*
7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	2757	6	Aad25729 Human cyc
2	654.4	24.2	2516	5	Aas63653 DNA encod
3	577.4	21.4	2607	7	Abz80565 Nucleotid
4	573.6	21.2	3811	5	Aas91658 DNA encod
5	569.6	21.1	4238	9	Adb53355 Primary r
6	518	19.2	2244	5	Aas76156 DNA encod
7	518	19.2	2244	5	Aas76184 DNA encod
8	223	8.3	3275	4	ABL19457 Drosophil
9	176.4	6.5	2500	9	Adg3243 Cyclic nu
10	160.6	5.9	289	5	Aas75291 DNA encod
11	136.2	5.0	2109	4	ABL18085 Drosophil
12	132.8	4.9	3486	9	Adb58492 Human CNG
13	131.6	4.9	1995	7	Aad56241 Rat CNG c
14	131.6	4.9	1995	7	Aad56239 Rat CNG c
15	129	4.8	526	4	Abag1898 Human foe
16	129	4.8	526	4	AAI41823 Probe #10
17	129	4.8	526	4	AAK36108 Human bon
18	129	4.8	526	4	AAK10209 Human bra
19	129	4.8	526	4	ABS35801 Human liv
20	128.4	4.8	1995	7	Aad56242 Rat CNG c
21	128.4	4.8	1995	7	Aad56240 Rat CNG c
22	127	4.7	127	4	ABA74393 Human foe
23	127	4.7	127	4	AAI54858 Probe #23

24	127	4.7	127	4	AAK49030	Aak49030 Human bon
25	127	4.7	127	4	AAK22857	Aak22857 Human bra
26	127	4.7	127	4	ABS48687	Abz48687 Human liv
27	124.4	4.6	5133	4	ABL14931	Abi14931 Drosophil
28	120.6	4.5	5692	4	ABL19456	Abi19456 Drosophil
29	116.8	4.3	1989	7	ABX94804	Abx94804 Bovine CN
30	115.2	4.3	1989	7	ABX94805	Abx94805 Bovine CN
31	113.6	4.2	1989	7	ABX94806	Abx94806 Bovine CN
32	111.2	4.1	1995	4	AAQ09558	Aaq09558 Human tra
33	111.2	4.1	1995	6	ABQ78297	Abq78297 Nucleotid
34	111.2	4.1	1995	7	ABS58301	Abz58301 cDNA enco
35	111.2	4.1	1995	7	ABZ80563	Abz80563 Nucleotid
36	111.2	4.1	2111	7	ABX56269	Abx56269 Human NOV
37	111.2	4.1	2190	6	ABA00289	Abz00289 Variant H
38	111.2	4.1	12017	7	ABS58302	Abz58302 Novel hum
39	109.6	4.1	2186	6	ABA00288	Abz00288 HBMYCNG C
40	109.6	4.1	3080	7	ACC43832	Acc43832 Nucleotid
41	96.4	3.6	2909	4	ABL13353	Abi13353 Drosophil
42	86.8	3.2	1281	4	ABL06311	Abi06311 Drosophil
43	86.2	3.2	2223	2	AAQ29187	Aaq29187 cDNA enco
44	85.6	3.2	2223	2	AAQ80908	Aaq80908 Plasmodiu
45	83	3.1	372	5	AA575452	Aas75452 DNA encod

ALIGNMENTS

RESULT 1
AAD25729
ID AAD25729 standard; DNA; 2757 BP.

XX
AC AAD25729;

DT 26-MAR-2002 (first entry)

XX Human cyclic nucleotide-gated cation channel 3 beta subunit DNA.

XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
XX cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
XX male infertility; genetic defect; reporter-ligand interaction; CNG;
XX viral infection; cancer; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_feature 1...49

FT /tag= a

FT /note= "These bases are absent in the sequence shown as

FT SEQ ID NO:2 in Page 64-65 of the specification"

FT CDS 112..2541

FT /tag= b

FT /product= "Human CNG3B protein"

FT /note= "This region is specifically claimed in claim 4 as

FT SEQ ID NO:4"

FT misc_feature 2753..2757

FT /tag= c

FT /note= "These bases are absent in the sequence shown as

FT SEQ ID NO:2 in Page 64-65 of the specification"

XX WC200188090-A2.

XX 22-NOV-2001.

XX 15-MAY-2001; 2001WO-US015814.

XX 15-MAY-2000; 2000US-0204445P.

XX 14-MAY-2001; 2001US-00855828.

XX (ICAG-) ICAGEN INC.

XX Creech CD, Jegla TJ;

XX WPI; 2002-089847/12.

DR P-PSDB; AAE15982.
 XX New polypeptide, useful for screening for modulators of cyclic nucleotide-
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
 PT cation channel 3 beta subunit.
 XX Claim 4; Fig 2; 83pp; English.
 XX The invention relates to human cyclic nucleotide-gated cation channel 3
 CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 CC subunits that are expressed in retina. CNG3B polypeptides are useful for
 CC screening modulators of CNGs which are useful as contraceptives and for
 CC treating various disorders involving cation channels, e.g. vision
 CC disorders and male infertility. Polynucleotides of the invention are
 CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.
 CC Sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is a DNA encoding CNG3B protein
 XX Sequence 2757 BP; 946 A; 571 C; 581 G; 659 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 2703; DB 6; Length 2757;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATTTCTCTACCTTAAGCCAGCTCATAAATACAGAGGGTTTTCAGAACCACTCCAGAGA 60
 DB 50 CATTTCTCTACCTTAAGCCAGCTCATAAATACAGAGGGTTTTCAGAACCACTCCAGAGA 109
 QY 61 AGATGTTTAAATCGCTGCAAAAGTCAACAGGTTGAAGCCCTATAGGAGAGAAACAATGAGA 120
 DB 110 AGATGTTTAAATCGCTGCAAAAGTCAACAGGTTGAAGCCCTATAGGAGAGAAACAATGAGA 169
 QY 121 ATGACAAAGTCTCGTGGGATGAGAGAGCTCTCACCAGTAATCACTCTCAGCAAA 180
 DB 170 ATGACAAAGTCTCGTGGGATGAGAGAGCTCTCACCAGTAATCACTCTCAGCAAA 229
 QY 181 CCACAGCAGGAGAAACAAAGGTTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAG 240
 DB 230 CCACAGCAGGAGAAACAAAGGTTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAG 289
 QY 241 TCAGTCTGAGAGCCACACACCACTACAGCAAACTCTCAGAGAAATTCCTCTG 300
 DB 290 TCAGTCTGAGAGCCACACACCACTACAGCAAACTCTCAGAGAAATTCCTCTG 349
 QY 301 GAGATCTGACCAACAAACCTGACCTCTCAAAATGAGAGAGAACTCTGGAACAGTGCAG 360
 DB 350 GAGATCTGACCAACAAACCTGACCTCTCAAAATGAGAGAGAACTCTGGAACAGTGCAG 409
 QY 361 AGCAGAGGAAATGAGCCCGGAGAAAGAGTCCAAACAGCCCAACAAACCGGCTG 420
 DB 410 AGCAGAGGAAATGAGCCCGGAGAAAGAGTCCAAACAGCCCAACAAACCGGCTG 469
 QY 421 CAGCTCTGTTTAAATGAGTATGCCGATGCCAGTACCAACTGGTCAAAAGAGATGC 480
 DB 470 CAGCTCTGTTTAAATGAGTATGCCGATGCCAGTACCAACTGGTCAAAAGAGATGC 529
 QY 481 GTCAAGAGAAACGCTCTTACAGAGAAAGTTGGTAGAGGAGATCTCTCTCACCAGAG 540
 DB 530 GTCAAGAGAAACGCTCTTACAGAGAAAGTTGGTAGAGGAGATCTCTCTCACCAGAG 589
 QY 541 CCAGCCCAACAACTGCAAGCCCGGCTGTACCACAGTAAAGAGAGCGATGATAAGC 600
 DB 590 CCAGCCCAACAACTGCAAGCCCGGCTGTACCACAGTAAAGAGAGCGATGATAAGC 649
 QY 601 CAACAGAACATTACTACAGGCTGTGTTGGTTCAAAGTCAAAAGATGCGCTTTTAAACAGAGT 660

DB 650 CAACAGAACATTACTACAGGCTGTTGTGTTCAAAGTCAAAAGATGCGCTTTTAAACAGAGT 709
 QY 661 ACTTAAAGCGAATTAAACTTTCAAACAGCATAGATTATACACAGATGAGCTCTATCTCC 720
 DB 710 ACTTAAAGCGAATTAAACTTTCAAACAGCATAGATTATACACAGATGAGCTCTATCTCC 769
 QY 721 TGTGGCTCTGCTGTGTCACCTCTTGCTATATACTGGAACCTGCTGGTTTATACCACTGCGCC 780
 DB 770 TGTGGCTCTGCTGTGTCACCTCTTGCTATATACTGGAACCTGCTGGTTTATACCACTGCGCC 829
 QY 781 TGTCTCTCCCATATCAAAACCGCAGACAACTACTCTGCTTATGCGGACATCATAT 840
 DB 830 TGTCTCTCCCATATCAAAACCGCAGACAACTACTCTGCTTATGCGGACATCATAT 889
 QY 841 GTGATATCATCTACCTTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGAAGAG 900
 DB 890 GTGATATCATCTACCTTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGAAGAG 949
 QY 901 GAGGACACATAATAGTGGATTCAAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAT 960
 DB 950 GAGGACACATAATAGTGGATTCAAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAT 1009
 QY 961 TTCAGTTGGATGTCGATCAATTAATACCAATTTGATATTTGCTTACCTCTCTTTGGGTTTA 1020
 DB 1010 TTCAGTTGGATGTCGATCAATTAATACCAATTTGATATTTGCTTACCTCTCTTTGGGTTTA 1069
 QY 1021 ATCCATGTTTAGACAAATAGGATGTTTAAAGTACACTTCTTTTGAATTTATCATC 1080
 DB 1070 ATCCATGTTTAGACAAATAGGATGTTTAAAGTACACTTCTTTTGAATTTATCATC 1129
 QY 1081 ACCTAGAGTCTTAATGGAACAAAGCATATATCTACAGAGTTTATTCGAAACAACTGATACT 1140
 DB 1130 ACCTAGAGTCTTAATGGAACAAAGCATATATCTACAGAGTTTATTCGAAACAACTGATACT 1189
 QY 1141 TGTGTTTAAATCTGACATTAATAGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGAA 1200
 DB 1190 TGTGTTTAAATCTGACATTAATAGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGAA 1249
 QY 1201 TTGGCACTACTAGATGGGTGATGATGGGAGGAAACAGATATCTGAGATGTTTATTTAT 1260
 DB 1250 TTGGCACTACTAGATGGGTGATGATGGGAGGAAACAGATATCTGAGATGTTTATTTAT 1309
 QY 1261 GGCGAGTTGGAATTTAAATTAATACCATTTGGTGGCTTCCAGAACCAAACTTTATTTGAAA 1320
 DB 1310 GGCGAGTTGGAATTTAAATTAATTAATTAATTAATTAATTAATTAATTTGAAA 1369
 QY 1321 TTGTTTTTCAACTCTGAAATTTTTTTCTGGAGTTTTTCTGTTCTCCAGTTTAAATGGTC 1380
 DB 1370 TTGTTTTTCAACTCTGAAATTTTTTTCTGGAGTTTTTCTGTTCTCCAGTTTAAATGGTC 1429
 QY 1381 AGATGAGAGATGATGATGGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGCATGG 1440
 DB 1430 AGATGAGAGATGATGATGGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGCATGG 1489
 QY 1441 ATGACACCAATGCTCTACATGACAACTTACTCCTTAACTTTGCAAAAGCGAGTTC 1500
 DB 1490 ATGACACCAATGCTCTACATGACAACTTACTCCTTAACTTTGCAAAAGCGAGTTC 1549
 QY 1501 GGACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTA 1560
 DB 1550 GGACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTA 1609
 QY 1561 AGACCCCTACCAACTACCGTCCAGTTAGCCCTCGCCATTTGATGTAATTCAGCATCATCA 1620
 DB 1610 AGACCCCTACCAACTACCGTCCAGTTAGCCCTCGCCATTTGATGTAATTCAGCATCATCA 1669
 QY 1621 GCAAAAGTGCATTTGTTCAAGGGTGTGATACACAGATGATTTTATGACATGTTGCTAAGAT 1680
 DB 1670 GCAAAAGTGCATTTGTTCAAGGGTGTGATACACAGATGATTTTATGACATGTTGCTAAGAT 1729
 QY 1681 TGAATTCGCTCTCTATTTGCTGCTGATCTTTGCTGCAAAAGCGAGAAATTTGGCAAGG 1740

Db 2489 GCATCGCCCTATCAGGGCCCTCGGCTCCACTACTCGGTTTACGATGGCTGGGAAACAGT 2548
 QY 1242 TATCTCAGATGTTATTATTTGGCAGCTTCCAACTTTAAATACCATTTGGTGGCTTCCAGAA 1301
 Db 2549 TATATTGCTGTTACTACTTGTCTGAAGACCTCATCACCATCGGGGGGCTGCTGAC 2608
 QY 1302 CCACAAAATTATTTGAATTTGTTTTCATCTTTTCACTTTTTCGAGTTTTCGAGTTTTCG 1361
 Db 2609 CCCAAGACACTCTTTGAAATTTCTTCCAGCTGCTGAAATTTTTCACGGGGCTCTTTGCT 2668
 QY 1362 TTCTCCAGTTTAAATTTGGTTCAGATGAGATGATGTTGGAGCAGCTTACAGCAATCAGAAC 1421
 Db 2669 TTCTCTGATGATCGACAGATGAGATGATGTTGGGGCGCCACCGCGGACAGACC 2728
 QY 1422 TACTTCCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1481
 Db 2729 TACTACCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2788
 QY 1482 CTGTGCAAAAGCGAGTTCCGACTTGGTATGATGATGATGATGATGATGATGATGATGATGAT 1541
 Db 2789 TCCGTGCAAGACCGCTCAAGACCTGGTACGATGATGATGATGATGATGATGATGATGATGATGAT 2848
 QY 1542 GATGAGTCTGATTTGCTTTAAGACCCCTACCACTACGCTCCAGTTAGCCCTCGCCATTGAT 1601
 Db 2849 GATGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2908
 QY 1602 GTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1661
 Db 2909 GTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2968
 QY 1662 TATGAT 1721
 Db 2969 TTTGAT 3028
 QY 1722 AAGGAGAAATTTGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1781
 Db 3029 AAGGGGAGATCGGCGGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3088
 QY 1782 GGCCTGAT 1841
 Db 3089 GGCCTGAT 3148
 QY 1842 AGCCTTTAGCAGCAGGAGGAGGAAACCGTCCGATGATGATGATGATGATGATGATGATGATGATGAT 1901
 Db 3149 AGCTGCTGCTGTTGGGGCGGAAACCGGCGACCGGCGACGCTGATGATGATGATGATGATGATGAT 3208
 QY 1902 GCCATCTTTTAACTTACGACAAAGACCGTCCGATGATGATGATGATGATGATGATGATGATGATGAT 1961
 Db 3209 ACCACCTTTTCACTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3268
 QY 1962 TCTGAAAGGATCTCTATGAAAGACCGCAGTGTCTTTTAAAGCAGAGGCTTAAGACCGCA 2021
 Db 3269 TCTCAGAGTTTACTCCGGAAGAAAGCCAGCGCATGCTGAGACCAACATAGCCCAAG 3328
 QY 2022 GAAG 2025
 Db 3329 GAGG 3332

RESULT 5
 ADB53355
 ID ADB53355 standard; DNA; 4238 BP.
 XX AC ADB53355;
 XX DT 04-DEC-2003 (first entry)
 XX DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3897.
 XX KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
 XX KW toxicity marker; toxicity progression; drug screening;
 XX KW primary rat hepatocyte toxicity modelling; gene; ds.

OS Rattus norvegicus.
 XX WO2003065993-A2.
 XX 14-AUG-2003.
 PD
 XX
 PF
 XX 04-FEB-2003; 2003WO-US003482.
 XX
 XX 04-FEB-2002; 2002US-0353171P.
 PR 13-MAR-2002; 2002US-0363534P.
 PR 08-APR-2002; 2002US-0370248P.
 PR 10-APR-2002; 2002US-0371134P.
 PR 10-APR-2002; 2002US-0371135P.
 PR 10-APR-2002; 2002US-0371150P.
 PR 11-APR-2002; 2002US-0371413P.
 PR 19-APR-2002; 2002US-0373601P.
 PR 19-APR-2002; 2002US-0373602P.
 PR 22-APR-2002; 2002US-0374139P.
 PR 08-MAY-2002; 2002US-0378370P.
 PR 09-MAY-2002; 2002US-0378652P.
 PR 09-MAY-2002; 2002US-0378653P.
 PR 09-MAY-2002; 2002US-0378665P.
 PR 09-JUL-2002; 2002US-0394230P.
 PR 09-JUL-2002; 2002US-0394253P.
 PR 04-SEP-2002; 2002US-0407688P.
 PR 28-JAN-2003; 2003US-0442900P.
 XX
 (GENE-) GENE LOGIC INC.
 XX
 PA Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
 PI Blashoff M;
 XX
 DR WPI; 2003-731472/69.
 XX
 PT Determining if a compound induces a toxic effect on a tissue or cell, for
 PT identifying hepatotoxic compounds, comprises comparing a gene expression
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
 PT mean values.
 XX
 PS Claim 44; SEQ ID NO 3897; 874pp; English.
 XX
 CC The present invention describes a method for determining whether a
 CC compound induces a toxic effect on a tissue or cell. The method comprises
 CC preparing a gene expression profile of a tissue or cell sample exposed to
 CC the compound, and comparing the gene expression profile to a database
 CC comprising data or information on the Tox mean and non-Tox mean value.
 CC The method is useful for predicting or identifying at least one toxic
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The
 CC genes listed in the specification are useful as diagnostic or toxicity
 CC markers for the prediction or identification of the physiological state
 CC of tissue or cell sample that has been exposed to a compound, or to
 CC identify or predict the toxic effects of a compound or an agent. These
 CC may also be used as markers for monitoring toxicity progression or for
 CC drug screening. The present sequence represents a primary rat hepatocyte
 CC toxicity modelling related gene sequence from the present invention.
 XX
 SQ Sequence 4238 BP; 1129 A; 1107 C; 1313 G; 689 T; 0 U; 0 Other;

Query Match 21.1%; Score 569.6; DB 9; Length 4238;
 Best Local Similarity 64.6%; Pred No. 1.2e-110;
 Matches 848; Conservative 0; Mismatches 464; Indels 0; Gaps 0;
 QY 679 TTCACAAAGCATGATTCATACAGATCGACTCTATCTCTGTGGCTCTGTGTGCA 738
 Db 2277 TCCCCAGAGCATCGACCCACTGACCAACCTCATCTCTGTGGCTGTCTTCGTGG 2336
 QY 739 CTCCTTGCTTAACCTGGAACTGGTTTATACCACTGCGCTCGTCTCCCATCAAA 798
 Db 2337 TCCTGGCTTGAACCTGGAACTGCTGTGATCTCTGTGGCTGGCTTCCGTACAGC 2396
 QY 799 CGCAGACAAACATACACTACTCTGGCTTATTCGGACATCATATGTATCATCTTACCTTT 858
 Db 2397 GGGCAGACAAACATCCACCTCTGGCTGTCTATGATGAGTACTTGTGGGCTTCTATCTACCTCC 2456

QY	859	ATGATATGCTATTATTATCCAGGCCAGACTCCAGTTTGTAAAGAGGAGACATAAATAGTGG	918
Db	2457	TGGACATCACCGTGTTCCAGATGCGTCTCCAGTTGTCAAAGCGGGACATCATACAG	2516
QY	919	ATTCAATGAGCTAAGGAACACTACAGACATCTTACAAAATTTTCAGTTGGATGCGCAT	978
Db	2517	ATAAGAAGGAGATGCGTAATAATTACCTGAAGTCTCAAGATTTAAGATGGACTTGCTCT	2576
QY	979	CAATAATACCAATTGATATTGCTACTCTCTCTTTGGGTTTAAATCCAATGTTTAGAGCAA	1038
Db	2577	GCCTTTTGGCTTTGGATTTTCTCTACTTGAACCTTGGCGTGAACCCCTTCTTCGCTGC	2636
QY	1039	ATAGGATGTTAAAGTACACTTCATTTTGTGAATTTAAATCATCACATGAGTCTATAAGG	1098
Db	2637	CCGCGTCCCTGAAGTACATGGCCTCTCTTGAGTTTAATAACCGTCTGGAAAGCATCCTCA	2696
QY	1099	ACAAAGCATATATCTACAGAGTTATTGAAACAACTGGATACTTGTCTTTATTCTGCACA	1158
Db	2697	GCAAGCCTACGTTTACAGGTTATCAGGACCACCGCTACCTGCTGTATAGCTTGCAATC	2756
QY	1159	TTAATCGCTGTGTTTATTACTGGCGTTCAAACTATGAAGAAATTGGCACTACTAGATGG	1218
Db	2757	TCAACTCGTGTCTTTACTACTGGCGCTCGCGCTTCAGGGCATCGGTTCCATCTACTGG	2816
QY	1219	TGTATGATGGGAAGAAACAGATATCTGAGATGTTATTATTGGGCAGTTCGAACTTTAA	1278
Db	2817	TTTATGACGCGTGGGAACAGCTACATTCGATGCTACTGTGGTGTGAAAACCTCTCA	2876
QY	1279	TTACCATTTGTGGCTTCCAGAACCAAACTTTATTGAAATTTTTCAACTCTTCA	1338
Db	2877	TCACCATCGGAGACTGCCCCAGCCCCAGCGCTTTTGAGATGCTCTTCCAGCTGCTGA	2936
QY	1339	ATTTTTTTTTCTGGAGTTTGTGTTCTCCAGTTTAAATTTGGTTCAGATGAGAGATGTGATTG	1398
Db	2937	ATTATTTTACAGTGTTCTCGCTTCTCTGTGATGATTTGGACAGATGAGAGATGTGGTG	2996
QY	1399	GAGCAGTTACAGCCAAATCAGAACTACTTTCGCGCTGTCATGGATGATGACCATTTGCCATCA	1458
Db	2997	GGGCGCGCCAGGCGGACACGCTACTACCGCAGCTGCTATGGACAGCAGCGTGAAGTACA	3056
QY	1459	TGAACAATTTACTCCATTCCCTAAAACCTGTGCAAAAGCGAGTTTCGGACTTGGTATGAATATA	1518
Db	3057	TGAACTTCTACAGATCCCCAGGTCGTGTCAGAACCGCTCAAGACCTGGTACGAATACA	3116
QY	1519	CATGGGACTCTCAAAGAATGTTAGATGAGTCTGATTTTGCTTTAAGACCTTACCAACTACGG	1578
Db	3117	CCTGGCACTCACAAGGCAATGCTGGATGAGTCAGAGCTGATGGTTCAGCTTCCGGACAAGA	3176
QY	1579	TCCAGTTTAGCCCTCGCCATTGATGTAAGAACTTCAGCATCATCAGCAAAAGTCGACTTGTTC	1638
Db	3177	TGCGTCTGGACCTGGCCATTGACGTAACTACAACTTTGTCAGCAAAAGTGGCGCTCTTCC	3236
QY	1639	AGGTTGTGTATACACAGATGATTTATGACATGTTGCTTAAGATTTGAAATCCGTTCTCTATT	1698
Db	3237	AGGCTGCGACCGGCAGATGATCTTCACATGCTCAAGCCAGCTTCGCTCAGTCGTCTATCC	3296
QY	1699	TGCGTGTGTACTTTGTCTGCAAAAAGGAGAAAATTTGGCAAGAAAATGTATATCATCAAGC	1758
Db	3297	TACCAATGACTATGTGTGCAAGAGGGGAGATTTGGCCGAGAGATGATATTATATCCAGG	3356
QY	1759	ATGAGAAGTCCAAGTCTTTGGAGGCCCTGATGTTGCTATAAGTTCTGGTTACTCTGAAAG	1818
Db	3357	CGGGCAGGTGCAGGTGTGGGGCGCCAGATGAAAGGCTGTCTCTGGTACACTCAAG	3416
QY	1819	CTGGGTGCGTGTGGAATAATCAGCCCTTCTAGCAGCAGGAGGAGGAAAACCGTCGAACTG	1878
Db	3417	CCGNATCGGTGTTTGGAGAGATAGCTGTGGCTGTCTGGGGCGGTAAACAGGGCGACGG	3476
QY	1879	CCAAATGCGTGGCCCAACGGGTTTGGCAATCTTTTAACTCTTAGACAAAAGACCTTCCAG	1938
Db	3477	CCAAATGCGTGGCCCAACGGGTTTCCAAATCTCTTCAATCTCTGGATAAGAGGACTTGAATG	3536

QY		1939	AAATTCAGTGCATTATCCAGATTCTGAAGGATCCTCATGAAGAAAGCCAG	1990
DH		3537	AAGTTTTGTGTGCA ^T TACCCCTGAATCTCAGAAGTGCTCCGGAAGAAGGCCAG	3588

RESULT 6

XX	AAAS76156
XX	ID AAS76156 standard; cDNA; 2244 BP.
XX	AC AAS76156;
XX	DT 13-FEB-2002 (first entry)
XX	DE DNA encoding novel human diagnostic protein #11960.
XX	XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	XX food supplement; medical imaging; diagnostic; genetic disorder; ss
XX	XX Homo sapiens.
XX	XX W0200175067-A2.
XX	XX 11-OCT-2001.
XX	XX 30-MAR-2001; 2001WO-008631.
XX	XX 31-MAR-2000; 2000US-00540217.
XX	XX 23-AUG-2000; 2000US-00649167.
XX	XX (HYSE-) HYSEQ INC.
XX	XX Drmanac RT, Liu C, Tang YT;
XX	XX WPI; 2001-639362/73.
XX	XX P-PSDB; ABG11969.
XX	XX New isolated polynucleotide and encoded polypeptides, useful in
XX	XX diagnostics, forensics, gene mapping, identification of mutations
XX	XX responsible for genetic disorders or other traits and to assess
XX	XX biodiversity.
XX	XX Claim 1; SEQ ID NO 11960; 103pp; English.
XX	XX The invention relates to isolated polynucleotide (I) and polypept
XX	XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX	XX reaction (PCR) primers, oligomers, and for chromosome and gene map
XX	XX and in recombinant production of (II). The polynucleotides are all
XX	XX in diagnostics as expressed sequence tags for identifying express
XX	XX genes. (I) is useful in gene therapy techniques to restore normal
XX	XX activity of (II) or to treat disease states involving (II). (II) i
XX	XX useful for generating antibodies against it, detecting or quant
XX	XX polypeptide in tissue, as molecular weight markers and as a food
XX	XX supplement. (II) and its binding partners are useful in medical di
XX	XX of sites expressing (II). (I) and (II) are useful for treating di
XX	XX involving aberrant protein expression or biological activity. The
XX	XX polypeptide and polynucleotide sequences have applications in
XX	XX diagnostics, forensics, gene mapping, identification of mutations
XX	XX responsible for genetic disorders or other traits to assess biodi
XX	XX and to produce other types of data and products dependent on DNA
XX	XX amino acid sequences. AAS64197-AAS94564 represent novel human dia
XX	XX coding sequences of the invention. Note: the sequence data for th
XX	XX patent did not appear in the printed specification, but was obtain
XX	XX electronic format directly from WIPO at
XX	XX ftp://wipo.int/pub/published/pct/sequences

349 GAACAGTCCAGAGCAGAGGAAATGGACCCCGGGAAGAGAGTCCAAACAGCCCCACA

Db 83 GCAAACTATCAAGGACAGAAACCAACACCGCATGTTCTCACACACAGCCACAAA 142
QY 409 ACAACCGCTGAGCTCTGTTATAATAGATATGCCGATGCCAGCTACACAACTGG 468
Db 143 ACAACCGCTGAGCTCTGTTATAATAGATATGCCGATGCCAGCTACACAACTGG 202
QY 469 TGAAGAAGATGGTCAAGACAGCCCTCTACAGAAAGATGGTAGAGGAGATCTCT 528
Db 203 TGAAGAAGATGGTCAAGACAGCCCTCTACAGAAAGATGGTAGAGGAGATCTCT 262
QY 529 CCTCACCGAAGCCAGCCACAACTGCAAAAGCCAGCTGTACACAGTAAAGAAA 588
Db 263 CCTCACCGAAGCCAGCCACAACTGCAAAAGCCAGCTGTACACAGTAAAGAAA 322
QY 589 GCGATGATAAGCCACAGACAACTACTACAGCTGTTGGTTCAAAGTCAAAAGATGC 648
Db 323 GCGATGATAAGCCACAGACAACTACTACAGCTGTTGGTTCAAAGTCAAAAGATGC 382
QY 649 CTTTAAACAGATCTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACAGATC 708
Db 383 CTTTAAACAGATCTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACAGATC 442
QY 709 GACTATCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db 443 GACTATCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 502
QY 769 TACCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
Db 503 TACCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562
QY 829 CGGACATCATATGATATCATCTACCTTTATGATATGCTATTATCCAGCCAGCTCC 888
Db 563 CGGACATCATATGATATCATCTACCTTTATGATATGCTATTATCCAGCCAGCTCC 622
QY 889 AGTTGTAAAGAGGAGACATAATA 914
Db 623 AGTTGTAAAGAGGAGACATAATA 648

RESULT 7

AAS76184/c

ID AAS76184 standard; cDNA; 2244 BP.

XX AAS76184;

AC AAS76184;

DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #11988.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG11997.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 1; SEQ ID NO 11988; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2244 BP; 463 A; 592 C; 469 G; 720 T; 0 U; 0 Other;

QY Query Match 19.2%; Score 518; DB 5; Length 2244;

Db Best Local Similarity 94.7%; Pred. No. 8.5e-100;

QY Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 349 GAACAGTCCAGCAGCAGAGGAAATGGACCCCGGAAAGAGGTCCAAACAGCCACAAA 408

QY 2162 GCAAACTATCAAGGACAGAAACCAACACCGCATGTTCTCACACACAGCCACAAA 2103

Db 409 ACAAAACCGCTGAGCTCTGTTATAATAGATATGCCGATGCCAGCTACACAACTGG 468

QY 2102 ACAAAACCGCTGAGCTCTGTTATAATAGATATGCCGATGCCAGCTACACAACTGG 2043

Db 469 TGAAGAAGATGGTCAAGACAGCCCTCTACAGAAAGATGGTAGAGGAGATCTCT 528

QY 2042 TGAAGAAGATGGTCAAGACAGCCCTCTACAGAAAGATGGTAGAGGAGATCTCT 1983

Db 529 CCTCACCGAAGCCAGCCACAACTGCAAAAGCCAGCTGTACCAACAGTAAAGAAA 588

QY 1982 CCTCACCGAAGCCAGCCACAACTGCAAAAGCCAGCTGTACCAACAGTAAAGAAA 1923

Db 589 GCGATGATAAGCCACAGACAACTACTACAGCTGTTGGTTCAAAGTCAAAAGATGC 648

QY 1922 GCGATGATAAGCCACAGACAACTACTACAGCTGTTGGTTCAAAGTCAAAAGATGC 1863

Db 649 CTTTAAACAGATCTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACAGATC 708

QY 1862 CTTTAAACAGATCTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACAGATC 1803

Db 709 GACTATCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768

QY 1802 GACTATCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1743

Db 769 TACCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828

QY 1742 TACCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1683

Db 829 CGGACATCATATGATATCATCTACCTTTATGATATGCTATTATCCAGCCAGACTCC 888

QY 1682 CGGACATCATATGATATCATCTACCTTTATGATATGCTATTATCCAGCCAGACTCC 1623

Db 889 AGTTGTAAAGAGGAGACATAATA 914

QY 1622 AGTTGTAAAGAGGAGACATAATA 1597

RESULT 8
 ABL19457
 ID ABL19457 standard; DNA; 3275 BP.
 XX
 AC ABL19457;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9844.
 XX
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW
 KW Drosophila; gene; ds.
 KW pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 XX
 WO200171042-A2.
 PN
 XX
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Claim 1; SEQ ID NO 9844; 2lpp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 3275 BP; 843 A; 849 C; 873 G; 710 T; 0 U; 0 Other;
 Query Match 8.3%; Score 223; DB 4; Length 3275;
 Best Local Similarity 48.7%; Pred. No. 3e-37;
 Matches 635; Conservative 0; Mismatches 665; Indels 3; Gaps 1;
 QY 712 TCTATCTCTGCTGCTTGTCTGCTCACTCTGCTATTAAGTGAAGTCTGTTTATAC 771
 DB 1552 TCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1611
 QY 772 CACTGCGGCTCTCTTCCATATCAACCGCAGACAACTACTGCTTATTCGG 831
 DB 1612 CGCTGGGCTCTGCTTCCCTTTCAACCAAGGAGAACCAATATCTGGCTGGCTGGC 1671
 QY 832 ACATCATATGATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGATCCAGT 891
 DB 1672 ACTTTGGCTGACATCATATATCTACTGGAATGGTCTCTTTAAACATCGGGTTATGT 1731
 QY 892 TTGTAAGAGGAGGAGACATATAGTGGATTCAAAATGAGCTAAGGAAACACTACAGGACTT 951
 DB 1732 ACCTTTTGAGGATCTGGGTGAAAACAGACACCTCACCAGAAAGTACATCGAA 1791
 QY 952 CTACAAAATTTTCAGTGGATGCGCATCAATTAACATTTGATTTGCTACCTCTCT 1011
 DB 1792 AACTGCACTTTAAGCTGATCTGCTGGCCCTTCTCCGCTGGAGTATTTACTTTAAAC 1851

QY 1012 TTGGGTTTAAATCCAAT--GTTTAGCAAAATAGGATGTTAAAGTACACATTTCAATTTTGG 1068
 DB 1852 TCGGAACACAGGCGGTTTGGTTGGCTTTTCCAGGTTCTTTAAGATTCAGAGCTTCTGGG 1911
 QY 1069 AATTAAATCATCACTAGAGTCTATAATGGAACAAAGCATATATCTACAGAGTATTTCGAA 1128
 DB 1912 AAGTGTTCGGCTTTGGATCGAGTATATCTCTCCGCACTTTGTTTCGAGTGGCCAAA 1971
 QY 1129 CAATGGATCTGCTGTTTATCTGCACATTAATGCTGTTGTTTATTTACTTGGCTTCAA 1188
 DB 1972 CCCTAACTTACATGCTCTACATGATCCACATCAGGCTGCTCTCTACTACGCTATAGT 2031
 QY 1189 ACTATGAAGAAATGGCACTACTAGATGGGTGATGATGGGAAGGAAACGAGTATCTGA 1248
 DB 2032 ACTACAGGCTCTGGGACAGAAATCGTTGGGTCTTCAGCGGCAAGGCAATCCCTATGTAA 2091
 QY 1249 GATGTTATTTGGGCGAGTTCGAACCTTTAATTACCATTTGGTGGCTTCCAGAACCAAAA 1308
 DB 2092 GGTGCTTTGCTTTTGGCCACCAAGACGGCACTTCGATAGGAAAAAACCAGCGGAC 2151
 QY 1309 CTTTATTTGAAATGTTTTCAACTCTTTGAAATTTTTTTCTGAGTTTTTTGTGTTCTCCA 1368
 DB 2152 GTCAGGAGAGTACGCTCTTCATGACGGTGGCTGGCTAATGGCGCTCTTTGTTGGCTC 2211
 QY 1369 GTTTAATTTGTCAGATGAGAGATGTGATGGAGCAGCTACAGCAATCAGAACTACTTCC 1428
 DB 2212 TGCATTATCGGTTCAGATCAGGATATCATCTCGACAGCCACTCGAATTAAGCATGATC 2271
 QY 1429 GCGCTGCTGATGGATGACACACCATTCCTACATGAACAATTTACTTCCATCTCTAACT 1488
 DB 2272 GCGAGCTGGAGATGAGACACTGGAGTACATCGAGCGCTCAATCTCTCGAGGAGTGC 2331
 QY 1489 AAAAGCGAGTTGGGACTTTGGTATGAATATAATGGGACTCTCAAGAAATGCTAGATGAGT 1548
 DB 2332 AGTCGAGGTCAAAATGTTGGTTCCAGTTTACATGGAGCAGCAGCGCACTTTTGGATGA 2391
 QY 1549 CTGATTTGTTAAGACCTTCCAACTACGCTCCAGTTCAGCTTCCCTTCCCTTATGATGA 1608
 DB 2392 CCAACATATGATGATGCTTTGGCCATCAATTTGAAACCGATATCGCCATCTCCGTGACA 2451
 QY 1609 TCAGCATCATCAGCAAAAGTTCGACTTTGTTCAAGGGTTGTGATACACAGATGATTTATGACA 1668
 DB 2452 TCCAAACGCTCTCCAAAGGTGCAACTCTTTGCTGATTCGAGGAGGCTTTTACTCAGAGATC 2511
 QY 1669 TGTGCTAAGATGAATTCGGTCTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728
 DB 2512 TGGTCTTAAACTAAGGCGAGTCAATTTTCCAGGAGATTTCTGTTCCGCCAAAGCGC 2571
 QY 1729 AAATTTGGCAAGGAAATGTATATCATCAAGCATGGAGAAAGTCCAAAGTTCTTTGGAGGCCCTG 1788
 DB 2572 AAGTGGCAGAGAGATGATATATCTGAACTGGGACAGGTTTCAAGTATGGGTGGTCTCA 2631
 QY 1789 ATGGTACTAAAGTCTGGTTACTCTGAAAGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1848
 DB 2632 GTAGCGATGTAGTGTGGGCACTCTAAACGAAAGGTTTCGGTGTTCGGGGAGATCAGTGTGC 2691
 QY 1849 TAGCAGCAGGAGGAGAAACCGTTCGAACCTGCAATGTTGGTGGCCCAACGCGGTTTGGCAATC 1908
 DB 2692 TGGGAATAATGGAGCCGATCGAGAAACAGAGATGTCGATCCAGAGGCTACTCCAACC 2751
 QY 1909 TTTTAACTCTAGACAAAAAGCCCTCCAAAGAAATTTCTAGTGCATTTATCAGATTTCTGAAA 1968
 DB 2752 TGTTCGTGCTGCTCAATCGGATTTAAACGAGTCAATTCCTCTACTATCCAGCGGCCAGG 2811
 QY 1969 GATTCCTCATGAAGAAAGCCAGATGCTTTTAAAGCAGAGGC 2011
 DB 2812 CGATTTCTAAAAGCGTCTCGTCACTAATGCGAAAAAATGC 2854

RESULT 9
 ADD93243
 ID ADD93243 standard; cDNA; 2500 BP.
 XX

AC ADD93243;
 XX 29-JAN-2004 (first entry)
 XX Cyclic nucleotide gated channel alpha 1 coding sequence.
 DE ss; gene; Cyclic nucleotide gated channel alpha 1;
 KW central nervous system; CNS; eye; blood-brain barrier;
 KW blood-retina barrier; angiogenesis; revascularisation;
 KW retinal pigment epithelium; RPE; neurosensory retina; choroidea;
 KW age-related macular degeneration; AMD; diabetic retinopathy;
 KW Alzheimer's disease; Parkinson's disease; depression; bipolar disorder;
 KW schizophrenia; amnesia; headache; stroke; insomnia; alcohol abuse;
 KW anxiety; chronic pain; retinal blastoma; primary retinal detachment
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX 25..2097
 XX CDS /tag= a
 XX /product= "Cyclic nucleotide gated channel alpha 1"
 XX W02003087368-A2.
 XX
 XX 23-OCT-2003.
 XX
 XX 16-APR-2003; 2003WO-EP004003.
 XX
 XX 18-APR-2002; 2002EP-00008761.
 XX 05-DEC-2002; 2002US-0431173P.
 XX
 XX (LYNK-) LYNKEUS BIO TECH GMBH.
 XX
 XX Drumm K, Schloer SH, Goehring F;
 XX WPI; 2003-845328/78.
 XX P-PSDB; ADD93244.
 XX
 XX Treating central nervous system and/or eye disorders comprises
 XX administering to a subject a composition comprising a compound that
 XX modulates a target gene or gene product, outside the blood-brain and/or
 XX blood-retina barriers.
 XX
 XX Claim 19; SEQ ID NO 1; 91pp; English.
 XX
 XX This sequence encodes the human cyclic nucleotide gated channel alpha 1
 XX protein. This cDNA may be targeted in the method of the invention for
 XX treating a disorder of the central nervous system (CNS) and/or the eye.
 XX The method comprises administering to a subject a composition comprising
 XX a compound capable of modulating a target gene or gene product in a
 XX therapeutic amount, where the composition is administered outside the
 XX blood-brain and/or the blood-retina barriers. The composition is in a
 XX designed form to be introduced into the cells or tissue of the CNS or eye
 XX by a suitable carrier, characterized by the application occurring outside
 XX the blood-brain or blood-retina barriers. It is also designed for
 XX systemic administration or for administration by iontophoresis, or for
 XX reticular application or as eye drops. The compound, nucleic acid
 XX molecule or vector is useful for the preparation of a composition for
 XX treating, preventing and/or delaying a disorder of the CNS and/or the
 XX eye, e.g. related to angiogenesis and/or neovascularisation, retinal
 XX pigment epithelium (RPE), neurosensory retina and/or choroidea and wet
 XX age-related macular degeneration (AMD) or diabetic retinopathy. The
 XX compound may also be used as a lead compound in drug discovery and
 XX preparation of drugs or prodrugs. The nucleic acid molecule and
 XX polypeptide are also used for the validation of test substances, lead
 XX compounds, drugs and prodrugs for the treatment of the disorder mentioned
 XX above or for the identification and isolation of downstream genes, which
 XX respond to modulation of a gene comprising the nucleic acid molecule or
 XX its encoded gene product. The method is used for diagnosing, preventing
 XX or treating the disorder cited above, which may include Alzheimer's
 XX disease, Parkinson's disease, depression, bipolar disorder,
 XX schizophrenia, amnesia, headache, stroke, insomnia, alcohol abuse,
 XX anxiety, chronic pain, retinal blastoma, primary retinal detachment or

CC age-related macular degeneration.
 XX
 XX Sequence 2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;
 SQ
 Query Match 6.5%; Score 176.4; DB 9; Length 2500;
 Best Local Similarity 49.6%; Pred. No. 2.1e-27;
 Matches 617; Conservative 0; Mismatches 591; Indels 36; Gaps 5;
 QY 802 CAGACACATACACTACTGCGCTATTCGCGACATCATATGTGATATCATCTACCTTTATG 861
 DB 605 CTGATTACCTAGAAATATGGCTCATTTTGGATTAGCATATCAGACATAGTCTATTAATCG 664
 QY 862 ATATGCTATTATTCAGCCAGACTCCAGTTTGTATAGAGGAGGACATATAATAGTGGATT 921
 DB 665 ATATG---TTTGTACGACACAGGAGGTTTACCTAGACAGGAGCTGCTGTTAAGGAAG 721
 QY 922 CAATGAGCTAGGAAACACTACAGACTTCTACAAAATTTTCAGTTGGATGTCGATCAA 981
 DB 722 AACTTAACTCATATAATAATAATCCAACTTGCATTTTAACTTGTATGTTCTGTAC 781
 QY 982 TAATACATTTCATATTTCTTACCTCTCTTTGGGTTTA---ATCCAATGTTTAGAGCA 1038
 DB 782 TGNATCAACTGATTTGCTGATTTTAAGTTAGGTGGAACTATCCAGAAATAGATTAA 841
 QY 1039 ATAGATGTTAAAGTACACTTCAATTTTGTGAATTTAATCATCACCCTAGAGTCTATAATGG 1098
 DB 842 ACAGGTTGTTAGGTTCTCTCGTATGTTTGTAGTTCTCCAGAGAACAGAAACAAGGACAA 901
 QY 1099 ACAAGCATATATCTACAGAGTTTTCGACAACTGGATACTTGTCTGTTTATTCTGCA 1158
 DB 902 ACTATCCAAACATCTTCAGGATTTCCAACTTGTGTTATGTATATGTCATCATTTATCCACT 961
 QY 1159 TTAATGCCCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1218
 DB 962 GGAATGCTATGTTGTTCTACTCTATTTCTAAAGCTATTGGATTGGAATATGATACATGG 1021
 QY 1219 TGTA-----TGATGGGAAGGAAACAGGATATCTGAGATGTT 1254
 DB 1022 TCTACCTGATATTAATGATCTGAATTTGGCCGTTTGGCTAGAAATACCTATACAGCC 1081
 QY 1255 ATTATTGGGCACTTCCAACTTTTAATTCATTGTTGGGCTTCCAGAACCAACAACTTTAT 1314
 DB 1082 TTTACTGTTTACACTGACTTTGACTACCATTTGGTGAACACCCCTCCCTGAGGATTT 1141
 QY 1315 TTGAATTTGTTTCAACTCTTGAATTTTCTGGAGTTTGTGTTTCTCCAGTTTAA 1374
 DB 1142 CTGAGTATGTTCTTGTGGTGGTTGATTTCTTAATTTGGAGTGTAAATTTTGTCTACCATCG 1201
 QY 1375 TTGGTCAGATGAGAGATGTTGAGGAGCTACAGCCCAATCAGAACTACTTCCGCGCT 1434
 DB 1202 TTGGTAAATAGGTTCTATGATTTTCCAACTGAATGAGCCAGAGCAGAAATTCAGCAA 1261
 QY 1435 GAATGATGACACCACTTCCCTACATGAACAAATTAATCTCCATTTCTTAACTTTGTGCAAAAGC 1494
 DB 1262 GAATTTGATGCTCAAGCAATATATGCAATTTTCCAAATGTAAGCAAGATATGGAAGA 1321
 QY 1495 GAGTTTCGAGCTTGGTATCAATATACATGGGACTCTCAAGATCTAGATGAGTCTGATT 1554
 DB 1322 GGGTTTAAATGTTTGTACTCTGAGCAACAAACAAACAAAGTTGATGAGAAAGAG 1381
 QY 1555 TGCTTAAGACCTTACCACTACGCTCCAGTTTAGCCCTCGCCATTTGATGTAACCTCAGCA 1614
 DB 1382 TCTTAAAGTATCTACCTGATATACTAAGAGCAGAAATTTGCCATCAACGTTCACTTACACA 1441
 QY 1615 TCATCAGCAAGTTCGACTTGTTCAGGGTTGTGATACAGATCATTTATGACATGTTC 1674
 DB 1442 CATTAAAGAGGTACGCACTTTTCTGATTGTGAAGTGTGTTCTGTTGGTGGATGTCT 1501
 QY 1675 TAAGATTGAATCCGTTCTCTTATTGCTGCTGCTGTTGTTGCTGCAAAAGGAGAAATTG 1734
 DB 1502 TGAATTCGAACCCCAAGTCTTACAGTCTCTGAGATTATATTGCAAGAAAGGGGATATCG 1561
 QY 1735 CGAAGGAATGTATATCATCAAGCATCGAGAGTCCCAAGTCTCTTGGAGCCCTGATGGTA 1794

CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences

SQ Sequence 2109 BP; 485 A; 589 C; 605 G; 430 T; 0 U; 0 Other;

Query Match 5.0%; Score 136.2; DB 4; Length 2109;
 Best Local Similarity 46.4%; Pred. No. 6.5e-19;
 Matches 607; Conservative 0; Mismatches 678; Indels 24; Gaps 4;

730 TGCTTGCTCACTCTTGCTATAAAGTGAAGTCTGCTGTTTATACCACTGCGCTCTCTCC 789
 2 TGGTGTGTCCATGGCTTCTGTACAACTCTGGGTGATAATCTACCGCTTTCGCTCTCC 61
 790 CATATCAAAACCGCAGACAAATACACTACTGCTTATTCGGACATCATATGTGATCA 849
 62 AGGAGATCAATCGCGAAGCATGCGCAATTTGTTCTGTCTGACTACCTGCTCGACTTCC 121
 850 TCTACCTTTATGATATGCTATTATCCAGCCAGACTCCAGTTTGAAGAGAGAGACA 909
 122 TGTATCTGATCGATACTGT---TCCACTTTCGACCGGATACCTGGAGGACGGGGTGC 178
 910 TAATAGTGAATCAATGAGTAAAGAAACACTACAGGACTTCTCAAAATTTCAAGTTGG 969
 179 TGCAGACGAGCGCTTGAAGCTGCGCACCACTACATGAACCTGAGCATCTTACATCG 238
 970 ATGTGCGCATCAATATACCAATTTGATTTGTTGCTACTCTCTTTGGGTTTAAATCAATGT 1029
 239 ACTGCTGTGCTGCTGCTGCTGCTGCTTCTCTATTGCTGCTGCTTAACTCGATCC 298
 1030 TTAGAGCAATAGGATGTTAAAGTACACTTCAATTTTTTGAATTTAATCATCACTAGAGT 1089
 299 TCGCAGCTTCCGGCTGGTGAAGATCTACCGGTTCTGGGCTTCTATGATCGACCGAGC 358
 1090 CTATATAGCAAAAGCATATATCTACAGATTTATTCGAACACTGGATCTGCTGTTTA 1149
 359 GGCACACCAACTACCGCAACTGTTTCCGAGCACGCGCTCATCTACCTACCTGTTGGA 418
 1150 TTCTGCACATTAATCCCTGTGTTATTACTGGCTTCAAACTATGAGGAATTCGCACTA 1209
 419 TATTCAATGGACGGTGTCTTACCACATCATACAGAACAAATGGTTCGGATCAC 478
 1210 CTAGATGGGT-----GTATGATGGGGAAGAAACGAGTATCTGAGATGTT 1254
 479 GCAACTGGGTCTACCAAGCTCGGAGTCGGCGAGCTGGTCAAGCAGTATCTGCGAGAGT 538
 1255 ATTATGGGCGAGTTCGAATTTAATACCATTTGGTGGCTTCCAGAACCAAACTTTAT 1314
 539 ACTACTGTGACACCTGGCCCTGACCACTCGGGGATCTTCCCAAGCGCGCTCCAAAG 598
 1315 TTGAATTTGTTTTCAACTCTGAATTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTAA 1374
 599 GCGAGTACGTCTTTGTTATCTGAGCTGCTCTTTGGCTGATGCTCTTCCGCAAGGTAC 658
 1375 TTGTCAGATGAGAGATGATGAGGAGCTAGCAACATCACTCTTCGCGCGCT 1434
 659 TGGGCGAGTGGCCAAACATTGTGACGTGAGTGCAGCGCGCAAGAGGTTTCAAGCCA 718
 1435 GCATGGATGACACCAATTCCTTACATGAACAAATTAATCTTCTTAAACTTTGTGAAAAGC 1494
 719 AGCTGGATGGGTGAGACGTACATCGGATGCGAGCTGTGCGCAATCATCTGCGAGTGA 778
 1495 GAGTTCGAGCTTGTATGAATATACATGGGACTCTCAAGAACTAGATGAGTCTGATT 1554
 779 AGGTCAATCAATGGTTCGATTTACCTTGTGCTTACGCAAAATATGCTCGGACGAGGCGCG 838
 1555 TGCTTAAGACCCCTACCAACTAGCTAGCTTCAGTTTACCGCTCGCAATTTGATGTAATCAGCA 1614
 839 CCGTGTCTCTTCTCTGATTAATAAAGGCTGAATAGCAATTAAGCTCCATTTAGATA 898
 1615 TCATCAGCAAGTGCATTTGTTCAAGGGTTGTGATACACAGATGATTTATGACATGTTGC 1674
 899 CGCTCAAGCGGTGGAGATTTTCCAAAAACACAGAGCGCGCTTCTCTATGCGAACTGGTGC 958

QY 1675 TAAGATTGAATCCGTTCTCTATTATTGCTGCTGACTTGTCTGCAAAAGGGAGAAATTG 1734
 DB 959 TGCSCCTGAGGCCCGTGTCTCTTCGCCCCCGGACTACATCTCGAAGAGGGCGAGGTGG 1018
 QY 1735 GCAAGGAAATGTATATCATCAAGCATGGAGAACTCCAAGTTCTTGGAGGCGCTGATGGTA 1794
 DB 1019 GCAAGGAGATGTACATTTGTGAACCGAGGAGATTCAGAGTGGTGGCCGAC---AATGGAA 1075
 QY 1795 CTAAGATTCGTTACTCTGAAAGCTGGGTGCTGTTTGGAGAAATCAGCCTTCTAGCAG 1854
 DB 1076 AGACGGTGAATGGCTCCCTGAAGGCTGGTTCTTATTTGGCGAGATTAGTATACTCAATA 1135
 QY 1855 CAGG---AGGAGGAAACCGTCGAACCTGCCAATCTGGTGGCCACCGGTTTGCCCAATCTTT 1911
 DB 1136 TGGSCACCGCAGCAACCGAGCGCACAGCCAGCTTCGCTCAGTGGGATACAGGACCTCT 1195
 QY 1912 TAATCTTAGACAAAAGACCCCTCAAAGAAATTCAGTCAATTCAGATTTCGAAAGGA 1971
 DB 1196 TCCTCTCTGACAAAGAGGACATGTGGGACGTGCTGAAGGATATCCGCGCGCGGTGTTTC 1255
 QY 1972 TCCTCATGAAGAAAGCAGAGTCTTTTAAAGCAGAAAGCTAAGACCGC 2020
 DB 1256 GTCTGAGTCTGATAGCGGTCAAGCGATTGGAGNAATACAGAAAGGCCCC 1304

RESULT 12
 AAD58492

ID AAD58492 standard; DNA; 3486 BP.

XX AAD58492;

DT 04-DEC-2003 (first entry)

XX Human CNG channel alpha 3 potassium channel (KCNQ2) DNA.

Human; urological disorder; urinary incontinence; gene therapy; cancer;
 kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;
 urethra; overflow urinary incontinence; stress urinary incontinence;
 nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
 CNG channel alpha 3 potassium channel; KCNQ2; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 40..2124

FT /tag= a

FT /product= "Human CNG channel alpha 3 potassium channel"
 FT /note= "The CDS is referred to as SEQ ID NO:27 in the
 specification"

XX WO2003061573-A2.

XX 31-JUL-2003.

XX 16-JAN-2003; 2003WO-US001450.

XX 18-JAN-2002; 2002US-0349511P.

XX 28-FEB-2002; 2002US-0360500P.

XX 15-MAR-2002; 2002US-0365041P.

XX 19-APR-2002; 2002US-0374063P.

XX 14-AUG-2002; 2002US-0403468P.

XX 27-SEP-2002; 2002US-0414262P.

XX 21-OCT-2002; 2002US-0419986P.

XX 05-NOV-2002; 2002US-0423809P.

XX 26-NOV-2002; 2002US-0429797P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Silos-Santiago I, Karicheti V;

XX WPI; 2003-598705/56.

XX P-PSDB; AAB38591.

XX DR

XX Identifying a compound for treating urological disorders, for example
PT urinary incontinence by assaying the ability of the compound to modulate
PT the nucleic acid expression or polypeptide activity.
XX
PS Disclosure; Page 156-159; Opp; English.
XX
XX The present relates to a method for identifying a compound for treating
CC urological disorders e.g., urinary incontinence including overactive/
CC overactive bladder, overflow urinary incontinence, stress urinary
CC incontinence caused by dysfunction of the bladder, urethra or central
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC cancer of the prostate or kidney disorders. The method is also useful, for
CC modulating hyperplasia in a cell and treating a subject having a
CC urological disorder. The invention is also used in gene therapy. The
CC present sequence is human CNG channel alpha 3 potassium channel (KCNG2)
CC DNA
XX
SQ Sequence 3486 BP; 912 A; 866 C; 865 G; 843 T; 0 U; 0 Other;
Query Match 4.9%; Score 132.8; DB 9; Length 3486;
Best Local Similarity 49.2%; Pred. No. 3.9e-18;
Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;
QY 918 GATTCAAATGAGCTAAGCAACACTACAGGACTTCTACAAATTCAGTTGGATGCGCA 977
Db 742 GATACCAACAGGCTGCGCAGCATTAACAGACGACCGAGTTCAGCTGGATGTTG 801
QY 978 TCAATAATACCATTTGATATTGCTACTCTCTCTTTGGTTTA---ATCAATGTTTGA 1034
Db 802 TCCCTGGTCCCGACCGCTTACTTAAAGTGGGCAAACTACCCAGAAGTGGAG 861
QY 1035 GCAATAGAGTGTAAAGTACACTTCTTTTGAATTTAATCATCACTAGTCTATA 1094
Db 862 TTCAACCGCTTACTGAAATTTTCCCGCTCTTTGAATTTCTTGACCGACAGACAAG 921
QY 1095 ATGACAAAGCATATATCTACAGAGTTATTTCGAACAATCGATCTGCTTTATTCTG 1154
Db 922 ACCAACTACCCAAATGTTTCGAGTTGGGAATTTGTTGATCTTCATCATCATC 981
QY 1155 CACATTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGAAITGGCACTACTA 1214
Db 982 CACTGGAATGCTGTCATCTACTTTGCCATTTCCAAATTTCAATTTGTTGGACAGACTCC 1041
QY 1215 TGGTGT-----ATGATGGGAAGGAAGCAAGTACTCTGAGA 1250
Db 1042 TGGGTCTACCCAAACATCTAATCCAGAGATGGGCGCTCTCCAGAGTACTTTAC 1101
QY 1251 TGTATTATTGGGAGTTTGAACCTTAAATTAATTAATTTGTTGGCTTCCAGAACCAAACT 1310
Db 1102 AGTCTCTACTGTTCCACCTTGACCTTACCACCATTTGTTGAGACCCACCCCGTGAAA 1161
QY 1311 TTATTGAAATGTTTTCCTTGAATTTTCTGAGTTTGTGTTTCTCCAGT 1370
Db 1162 GATGAGGAGTATCTCTTTGTTGCTGATAGTCTTTGTTGGTGTCTGATTTTGGCACC 1221
QY 1371 TTAATTGTCAGATCAGAGATGTTGATTTGGAGCAGCTACAGCAATTCAGAACTCTCCG 1430
Db 1222 ATTTGGGCAATGGGCTCCATGATCTCGATATGATGCTCAGCGGAGAGTTCCAG 1281
QY 1431 GCTTCATGGAATGACACCATTCGCTACATGACAAATTAATCTCATCTTAACTTTGTGCA 1490
Db 1282 GCCAAGATGATTCCATCAAGCAGTACATGATGATGTTCCGAAAGTCCAGAGACTTGGAG 1341
QY 1491 AAGCGAGTTCGACTTGGTATGAATATACATGGGACTCTCAAGAAATCTAGATGAGTCT 1550
Db 1342 ACGGGGTTATCCGGTGGTTTGAATCTCTGTTGGGCAACAGAGACCGTGGATGAGAAG 1401
QY 1551 GATTTGCTTAAGACCTCACTACCTAGGTCAGTTAGCCCTCGCATTTGATGTAACATTC 1610
Db 1402 GAGGTGCTCAAGAGCTCCAGACAGCTGAAGGCTGAGATCGCCATCAACGTCACCTG 1461
QY 1611 AGCATCATCAGCAAGTACTTGTTCAGGGTGTGTATACACATGATTTATGACATG 1670

Db 1462 GACACGCTGAAGAAGTTCGCATCTTCAGGACTGTGAGCAGGCTGCTGTGGAGCTG 1521
QY 1671 TTGCTAAGATTAAGTCCGTTCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1730
Db 1522 GTGCTGAAGCTGCGACCCACTGTGTTGAGCCCTGGGATTATATCTGCAAGAGGAGAT 1581
QY 1731 ATTGCAAGGAATGATATATATCATCAAGCATGAGAGTCCAAAGTCTTTGAGGCGCTGAT 1790
Db 1582 ATTGGAAGGAGATGATATCATCAACAGAGGCAAGCTGGCCGTGTTGCTGATGATGGG 1641
QY 1791 GGTACTAAAGTTCTGGTTTACTCTGAAAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1849
Db 1642 GTACCCAGTTCGTTGTT---CTCAGCGATGCGAGTACTTCCGGGAGATCAGCATCTG 1698
QY 1850 ACCAGCAGAGAGAGAAACCGTCGAACTGC 1879
Db 1699 AACATCAAGGGGAGCAAGTCCGGGAACCGC 1728
RESULT 13
AAD56241
ID AAD56241 standard; DNA; 1995 BP.
XX
AC AAD56241;
XX
DT 07-AUG-2003 (first entry)
XX
DE Rat CNG channel alpha subunit mutant DNA #2.
XX
KW Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
KW cyclic nucleotide-gated channel; CNG channel; mutant; gene; ds.
XX
OS Rattus norvegicus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1995
FT /tag= a
FT /product= "CNG channel alpha subunit mutant protein"
XX
PN WO2003038039-A2.
XX
PD 08-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-US034122.
XX
PR 26-OCT-2001; 2001US-0330663P.
PR 04-MAR-2002; 2002US-00087217.
XX
PA (APTU-) APTUS PHARM INC.
XX
PI Yao Y, Cao L;
XX
XX WPI; 2003-430510/40.
DR P-PSDB; AAE37221.
XX
XX New host cell comprising first and second nucleic acids with promoters
XX that encode exogenous G protein-coupled receptor and cyclic nucleotide-
XX gated channel, respectively, useful for identifying agents that modulate
XX GPCR activity.
XX
XX Claim 12; Page 86-89; 98pp; English.
XX
XX The invention relates to compositions and methods for identifying G
XX protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
XX mediated activities. The invention also provides an host cell comprising
XX first and second nucleic acids with promoters that encode exogenous G
XX protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
XX respectively. The host cells are useful for identifying agents that
XX modulate an activity mediated by a GPCR. The present sequence is rat CNG
XX channel alpha subunit mutant encoding DNA

CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel	
CC respectively. The host cells are useful for identifying agents that	
CC modulate an activity mediated by a GPCR. The present sequence is rat CNG	
CC channel alpha subunit wild-type DNA	
XX	
SQ	Sequence 1995 BP; 529 A; 460 C; 505 G; 501 T; 0 U; 0 Other;
Query Match 4.9%; Score 131.6; DB 7; Length 1995;	
Best Local Similarity 46.7%; Pred. No. 68-18;	
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;	
QY	714 TATCTCTCTGGCTCTTGTCTGCTCACTCTTGTCTATTAAGTGAAGTCTGTTTATACCA 773
DB	424 TATTACCGTGTGTTTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
QY	774 CTGCGCTGCTCTTCCCATATCAACCGGAGACACATACACTACTGCTTATTGGGAC 833
DB	484 GCCAGAGCCTGCTTCAGTGTATACAGAGAACTATTGTTGTTGTTGCTGCTGCTGCTG 543
QY	834 ATCATATGTATATCATCTACCTTTTATGATATGCTATTTATCCAGCCAGACTCCAGT 893
DB	544 TACTTCTCAGACACTGCTATATCGAGACCTCATCTTCGGCTGGCACAGC---TTC 600
QY	894 GTAAGAGGAGGACATAATAGTGGATTCAAATGAGCTAAGGAACTACAGGACTTCT 953
DB	601 CTAGAACAGGGGCTCTTGGTCAAGATCCCAAGAAATTCGAGACAACTATATTACACT 660
QY	954 ACAAATTTCAAGTGGATGCTGATCAATAATACCAATTTGATTTGCTACCTCTCTTT 1013
DB	661 TTCCAGTTCAAAATGAGTGGCTTCTATCAITTCACCTGACCTTATCTATTTTGTCTG 720
QY	1014 GGGTT---TAATCCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCATTTTGA 1070
DB	721 GGTATCCAGACGCTGAGGTAGCTTCAACCGTCTATTACACTTTGCCGCTATGTTGAG 780
QY	1071 TTTAATCATCCTAGAGTCTAATAGGACAAAGCATATATCTACAGAGTATTTCGAACA 1130
DB	781 TTCTTTGACCGCACTGAGACACGCCAGCTACCCCAACATCTTCGGAATCAGCAATCTG 840
QY	1131 ACTGGATPACTGTGTTTATTCTGCAATTAATGCTGTTGTTTATTACTGGGCTTCAAA 1190
DB	841 GTCTTTACATCTGTCATCCACTGGAATGCTTGTTATTATTATGTTATTCTTAAG 900
QY	1191 TATGAAGGAATTGG-----CACTACTAGATGGGTGTTATGAT 1226
DB	901 TCCATTGGCTTTGGAGTTGACACTGGGTTTACCCCAACATTACTGACCCGTGAATGCG 960
QY	1227 GGGAGGAACAGGATCTGAGATGTTATTATTGGGCACTTCGAACCTTTAATTACCA 1286
DB	961 TACCTGCTAGAGTACATTTACTGCTTTTACTGTTCCACACTGACCCCTCACCACT 1020
QY	1287 GGTGGCCTTCCAGAACCAAACTTTATTGAAATGTTTTTCAACTTTTGAATTTTTTT 1346
DB	1021 GGAGAGACACACACCCCTGTAAGGATGAGGATACCTATTTGTCATCTTTGACTTCTTG 1080
QY	1347 TCTGGATTTTGTGTTCTCCAGTTTAAATGGTCAGATGAGATGTTGTTGGAGCAGCT 1406
DB	1081 ATTGGTGTCTCATCTTTGCGCACTATTGTTGGAAATGTTGGCTCCATGATCTCAACATG 1140
QY	1407 ACAGCCAATCAGAACTACTTCCGCGCTGATGATGACACCACTTGCTTACATCAACAAT 1466
DB	1141 AATGCCACACAGCAGAGTCTCCAGGCCAAGATTGATGCTGTCAAACTACATGCACTTC 1200
QY	1467 TACTCCATTCCTAACTTTGTGCAAAAGCGAGTTCGGACTTGGTATGATATATACATGGAC 1526
DB	1201 CGAAAGGTTCAGAAAGACATGGAAGCAAGTCAATAATGGTTTGTACTCTTGTGGACC 1260
QY	1527 TCTCAAGAAATGCTAGATGATGCTGTTTGTCTTAAGACCTTACCACTACGGTCCAGTTA 1586
DB	1261 AATGAAGACAGTATGATGAACGAGAGTCTCCAGAACCTGCCAGCAAGCTCAGGGCT 1320
QY	1587 GCCCTCGCAATGATGTAATCTCAGCATCATCAGCAAAAGTGCAGCTTGTTCAGGGTGT 1646

DB	1321 GAGATAGCCATTAAATGTTCACTTGTCCACTCTGAAGAAAGTGGCATATTTCCAGGATTGT 1380
QY	1647 GATACACAGATGATTATGACATGTTGCTAAGATTGAATCCGTTCTCTATTTTGCCTGGT 1706
DB	1381 GAAGCTGGCCTACTGGTGGAACTGGTACTGAAGCTTCGCTCCTCAGTCTTTAGTCCCTGA 1440
QY	1707 GACTTTGCTGCAAAAAGGGAGAAATTTGCAAGAAATGATATATCATCAAGCATGGAGAA 1766
DB	1441 GATTATATTTGCGCTAAGGGGACATTGGCAAGAAATGTACATCATCAAGGAGGGCAAG 1500
QY	1767 GTCAAAGTTCTTGAGGCCCTGATGTTGCTACTAAAGTTCTGCT---TACTCTGAAAGCTGG 1822
DB	1501 TTGCAAGTGGTAGTGTATGATGTTGGCTGACTCATGATGCCTTGCTCTCAGCTGGAGCTGC 1560
QY	1823 GTCGGTGTGTTGGAGAAATCAGCCCTTTAGCAGCAGGAGGA--GGAAACCTGCGAAGTGC 1880
DB	1561 TTTGGTGAATAGTATCTTAACTTAAGGGTAGCAAAATGGGCAATCGACGTACTGCT 1620
QY	1881 AATGTGGTGGCCACGGGTTTGGCAATCTTTTAATCTAGACAAAAGACCCCTCCAAGAA 1940
DB	1621 AATATCGTAGCCTGGGCTACTCAGATCTCTTCTGTTGTCCAAGGACGATCTTATGGAA 1680
QY	1941 ATTCTAGTGCATTATCCAGATTCTGAAAGGATCTCATGAAGAAAGCCAGAGTCTTTTA 2000
DB	1681 GCTGTACTGATGATCTCTGATGCTCAAGAGTCTCTGGAGAACGGGTAGGAGATCCTG 1740
QY	2001 AAGCAGAGGCT 2012
DB	1741 ATGAAGGAAGGT 1752
RESULT 15	
ABA61898	
ID	ABA61898 standard; DNA; 526 BP.
XX	ABA61898;
AC	
XX	01-FEB-2002 (first entry)
DE	Human foetal liver single exon nucleic acid probe #10203.
XX	Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
OS	Homo sapiens.
XX	
PN	WO200157277-A2.
XX	09-AUG-2001.
PD	
XX	30-JAN-2001; 2001WO-US000669.
PF	
XX	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207458P.
PR	30-JUN-2000; 2000US-0060840P.
PR	03-AUG-2000; 2000US-0063236P.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	(MOLE-) MOLECULAR DYNAMICS INC.
PA	
XX	Penn SG, Hanzel DK, Chen W, Rank DR;
PI	WPI; 2001-483447/52.
XX	
DR	Human genome-derived single exon nucleic acid probes useful for analyzing
XX	gene expression in human fetal liver.
PT	
XX	Claim 1; SEQ ID NO 10203; 639pp + Sequence Listing; English.
PS	
XX	The invention relates to a single exon nucleic acid probe for measuring
CC	human gene expression in a sample derived from human foetal liver. The
CC	single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 526 BP; 174 A; 119 C; 99 G; 134 T; 0 U; 0 Other;

Query Match 4.8%; Score 129; DB 4; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	272	AGACAACTCTCCAAAGAAAAATTCCTCTGGAGATCTGACCAAAACCCCTGACCCCTCAAAA	331
Db	191	AGACAACTCTCCAAAGAAAAATTCCTCTGGAGATCTGACCAAAACCCCTGACCCCTCAAAA	250
QY	332	TCCACGACCACTGGAACAGTCCACAGCAGAGGAAATGGACCCCGGGAAGAAGG	391
Db	251	TCCACGACCACTGGAACAGTCCACAGCAGAGGAAATGGACCCCGGGAAGAAGG	310
QY	392	TCCAAACAG 400	
Db	311	TCCAAACAG 319	

Search completed: June 21, 2004, 19:01:03
Job time : 1020.37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:18:50 ; Search time 6748.81 Seconds
(without alignments)
11960.251 Million cell updates/sec

Title: US-09-855-828-2

Perfect score: 2703

Sequence: 1 cattctctaccttaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_estin:*

3: em_estin:*

4: em_estin:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	886.2	32.8	2056	11 AK040140	AK040140 Mus muscu
2	553	20.5	553	10 BF725470	BF725470 bx15c03.y
3	526	19.5	527	9 AL713036	AL713036 DRFZP686A
4	470	17.4	655	10 BB635459	BB635459 BB635459

C	5	430.2	15.9	437	10	BF725459
	6	402.4	14.9	881	10	BF725459
	7	363.8	13.5	1201	13	BE287002
	8	328.4	12.1	832	12	BI827605
	9	320.8	11.9	468	9	AA069559
	10	317	11.7	445	14	H53423
	11	308.4	11.4	978	13	BQ68992
	12	301.4	11.2	694	9	AI137778
	13	285.8	10.6	741	13	BI104558
	14	280.8	10.4	738	12	BI736222
	15	280.4	10.4	758	9	AV726367
	16	280	10.4	423	12	BM938767
	17	271.2	10.0	545	10	AA465556
	18	262.2	9.7	563	12	BG304577
	19	261.6	9.7	503	9	AI150392
	20	245.6	9.1	674	29	CC498739
	21	234	8.7	247	9	AA317961
	22	232.4	8.6	270	9	AA012972
	23	224	8.3	325	10	BE92488
	24	219	8.1	696	13	BM269181
	25	216.2	8.0	518	9	AV605886
	26	216.2	8.0	747	12	BI733974
	27	212.4	7.9	215	9	AA069498
	28	211	7.8	869	14	CD327412
	29	201.6	7.5	993	13	BI370500
	30	197.2	7.3	581	9	AV605887
	31	165.6	6.1	353	9	AI120448
	32	164	6.1	376	9	AI120239
	33	131.2	4.9	591	29	CC571022
	34	129.8	4.8	573	12	BM354832
	35	120.6	4.5	535	9	AL928461
	36	111	4.1	920	13	BU139545
	37	110.6	4.1	490	13	BQ639921
	38	109.2	4.0	584	12	BM82371
	39	106.8	4.0	819	13	BU287884
	40	105.6	3.9	1215	28	CC245670
	41	102.8	3.8	795	13	BU291723
	42	97.6	3.6	573	29	CG985260
	43	96.6	3.6	706	9	AJ442203
	44	94.4	3.5	800	29	CNS03HXC
	45	92.2	3.4	567	10	BF937274

ALIGNMENTS

RESULT 1
AK040140
LOCUS
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430069G05 product:cyclic nucleotide gated channel beta 3, full insert sequence.
ACCESSION AK040140
VERSION AK040140.1 GI:26087649
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
2056 bp mRNA linear HTC 19-SEP-2003

REFERENCE

1
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 20499374
MEDLINE 11042159
PUBMED

QY 2218 AACAAAGAAATGAGATTAACAAAGAAATGAAGTAAAGGAAAGAAATGAAG 2277
 DB 1044 GTTCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
 QY 2278 ATAAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2337
 DB 1104 AAAAGAGA-----AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149
 QY 2338 GTCTATTGCTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2397
 DB 1150 GTTCTATTACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1209
 QY 2398 CTTCTCGTCAATCACTTATCAGATGAGAGAGAGAGAGAGAGAGAGAG 2457
 DB 1210 ATGCGTATCAATTTGATCATCAGACATAG--TCCTGCTACTGAGACT 1268
 QY 2458 TTACTATTGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2517
 DB 1269 TCACTATCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1328
 QY 2518 ATAGCTAGTTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2577
 DB 1329 CTAGCTAATTCCTCAAGAGAG--TCCTGGAATTTAGCTTAATTAAGG 1386
 QY 2578 ACATGCTGGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
 DB 1387 ACCTCACTGGAGCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443

RESULT 2
 BF725470 553 bp mRNA linear EST 05-JAN-2001
 LOCUS bxl6c03.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo
 DEFINITION sapiens cDNA clone bxl6c03 5', mRNA sequence.
 ACCESSION BF725470
 VERSION BF725470.1 GI:12041381
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 553)
 Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
 NEIBANK: EST analysis and bioinformatics for ocular genomics
 Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
 Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 16 row: c column: 03
 Seq primer: M13Rpl reverse primer (ABI).
 Location/Qualifiers
 1..553
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="bxl6c03"
 /tissue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMBL10B"
 /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
 BX"

FEATURES

source

AL713036 527 bp mRNA linear EST 04-SEP-2003
 LOCUS DKFZP686A1695.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 DEFINITION DKFZP686A1695 5', mRNA sequence.
 ACCESSION AL713036
 VERSION AL713036.1 GI:19696392
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 527)
 Bloecker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and
 Wiemann,S.
 EST (Bloecker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and
 Wiemann,S.)
 JOURNAL Unpublished (1999)

full details of which are contained in the manufacturer's
 instruction manual (http://www.lifetech.com/). First
 strand synthesis was carried out using a Not I
 primer-adaptor
 [5'-pGACTAGTTCTAGATCCGAGCGGCGCC(T)15-3']. Not I/blunt
 end inserts were cloned into the Not I/EcoR V sites in the
 vector. EST analysis was performed on the unamplified
 library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 20.5%; Score 553; DB 10; Length 553;
 Best Local Similarity 100.0%; Pred. No. 6e-80;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1145 GTTATTCTGCACATTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTGG 1204
 DB 1 GTTATTCTGCACATTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTGG 60
 QY 1205 CACTACTAGATGGGTGTAAGATGGGGAAGAAACAGATATCTGAGATGTTATTATTGGGC 1264
 DB 61 CACTACTAGATGGGTGTAAGATGGGGAAGAAACAGATATCTGAGATGTTATTATTGGGC 120
 QY 1265 AGTTCCGAACCTTTAATTACCATTTGGTGGCTTCCAGAACCAAACTTTATTGAAATTGT 1324
 DB 121 AGTTCCGAACCTTTAATTACCATTTGGTGGCTTCCAGAACCAAACTTTATTGAAATTGT 180
 QY 1325 TTTTCAACTCTGTAATTTTTTTCTGAGATTTTTTCTGAGATTTTTTCTCCAGTTTAATTTGGTCA 1384
 DB 181 TTTTCAACTCTGTAATTTTTTTCTGAGATTTTTTCTGAGATTTTTTCTCCAGTTTAATTTGGTCA 240
 QY 1385 GAGAGATGTGATGGAGCAGCTACAGCAATCAGAACTACTTCCGCCCTGCATGGATGA 1444
 DB 241 GAGAGATGTGATGGAGCAGCTACAGCAATCAGAACTACTTCCGCCCTGCATGGATGA 300
 QY 1445 CACCATTCCCTACATGAACAATTAATCTCCATTCTTAAACTTTGTGCAAAAGCGAGTTCGGAC 1504
 DB 301 CACCATTCCCTACATGAACAATTAATCTCCATTCTTAAACTTTGTGCAAAAGCGAGTTCGGAC 360
 QY 1505 TTGGTATGAATATACATGGGACTCTCAAGAGATCTAGATGAGTCTGATTTGCTTAAGAC 1564
 DB 361 TTGGTATGAATATACATGGGACTCTCAAGAGATCTAGATGAGTCTGATTTGCTTAAGAC 420
 QY 1565 CTTACCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTAACCTTCAGCATCATCAGCAA 1624
 DB 421 CTTACCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTAACCTTCAGCATCATCAGCAA 480
 QY 1625 AGTCGACTTGTCAAGGTTGTTGATACACAGATGATTATGACATGTTGCTTAAGATTGA 1684
 DB 481 AGTCGACTTGTCAAGGTTGTTGATACACAGATGATTATGACATGTTGCTTAAGATTGA 540
 QY 1685 ATCCGTTCTCTAT 1697
 DB 541 ATCCGTTCTCTAT 553

RESULT 3

AL713036

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGAGTTAATAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda ϕ 101.

ORIGIN	Query Match	Best Local Similarity	Matches 553;	Conservative 0;	Mismatches 101;	Indels 3;	Gaps 2;
Qy	1140	TTGCGTTTATTCGACATTAATGCGTGTGTTTATCTACTGGCTTCAACATGAAAGGA	1199				
Db	1	TTGCTGTGTTCTCCGACATTAACGCCGTGTGTTTATCTGGGCTTCAGACTATGAAGGA	60				
Qy	1200	ATTGCCACTACTAGATGGGTGTATGATGGGAGGAACGAGTATCTCAGATGTTATATAT	1259				
Db	61	ATTGCTCAACTAAATGGGTCTATAATGTGTGAAGGCAACAAGTATCTCGATGCTTTTAT	120				
Qy	1260	TGGGAGTTCGAACCTTTAATTACCAATGTTGGGCTTCAGAACCAACAACCTTTATTTGAA	1319				
Db	121	TGGGAGTTCGAACCTTTAATTACTATCGGGGGCTTCCAGAGCCACAGACTTCATTTGAA	180				
Qy	1320	ATTGTTTTTCAACTCTTGAATTTTTTTTTCTGGAGTTTTTGTCTTCTCCAGTTTAAATGGT	1379				
Db	181	ATTGTTTTTCAATCTTGAATTTTTTCTCTGGGGTTTTTGTGTTTTCTCCAGCTTAAATGGT	240				
Qy	1380	CAGATGAGAGATGTGATTGGAGCAGCTACAGCCAATCAGAACTACTTTCGGGCGCTGCATG	1439				
Db	241	CAGATGCGTGTGTGATTGGGGGAGCAACAGCCAATCAGAACTACTTCCAAAGCGCTGCATG	300				
Qy	1440	GATGACACCAATTCCTACATGAACAATTAATCTCCATTTCCTAAACTTGTGCAAAAGCGAGTT	1499				
Db	301	GACCATATCATTTGCTACATGACAAATACTCTATTTCCTCAGAGTGTGCAGTATCGAGTT	360				
Qy	1500	CGGACTTGGTATGAATATATCATGGGACTCTCAAGAAATGCTAGATAGTCTGATTCGCTT	1559				
Db	361	CGGACTTTGGCTGGAAATATACATGGAATCTCAAGAAGAACTCTAGATGAGTCCAACTTCGCTT	420				
Qy	1560	AAGACCCCTACCAACTACGCTCCAGTTAGCCCTCGCCATTGATGTCAACTTCAGCATCATC	1619				
Db	421	GAGAACCTCCCGACAGCAATGCAGTTGTCTATTGGCCCTTGACATAAACTTCAGTATCATC	480				
Qy	1620	AGCAAGTTCGACTTGTTCACAGGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGA	1679				
Db	481	GACAAAGTGGAGTTTATTCAAGGGCTGTGACACACAGATGATTTATGACCTCTGCTAAGA	540				
Qy	1680	TTGAAATCCGTTCTCTATTGTCCTTGTTGATCTTTGCTGCAAAAGGAGAAATTTGCAAG	1739				
Db	541	TTGAAATCCACTATTTATTTTACTCTGGTGACTTGTCTGCAAAAGGAGAAATTTGGAAG	600				
Qy	1740	GAAATGTATATCATCAAGCATGGAGAGTCCAAAGTTCTTTGGAGGCCCTTGATGGTACT	1796				
Db	601	--AATGTACATCATCAA-CACGAGAGAGTCCAGTCTTTGGAGGCCCTTGATGGTGTCT	654				

RESULT 5	
BF725469/c	
LOCUS	
DEFINITION	linear mRNA
ACCSSION	437 bp
VERSION	bx16c03.x1 Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bx16c03 3', mRNA sequence.
KEYWORDS	
EST.	
SOURCE	BF725469.1 GI:12041380
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 437);
AUTHORS	Wistow,G.U., Bernstein,S., Behal,A. and Smith,D.
TITLE	NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL	Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT	Contact: Wistow G

Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 16 row: c column: 03
Seq primer: -21M13 forward primer (AB1).

FEATURES
source

```

/clone_lib="Human iris cDNA (Un-normalized, unamplified):
BX"
/notes="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript Plasmid System
full details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
(5'-GATAGTCTTGAATCGAGCGCGGCC(7)15-3'). Not I/blunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (INISC)."

```

ORIGIN

Query Match	15.98;	Score 430.2;	DB 10;	Length 437;
Best Local Similarity	99.3%;	Pred. No. 5.4e-60;		
Matches 432;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1821	GGGTGGGTGGTTTGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTGCC	1880	
DB	437	GGGTGGGTGGTTTGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTGCC	378	
QY	1881	AATGTGTGGCCCAACGGGTGGTTCGCAATCTTTTAATCTAGACAAAGAACCCTCGAGAA	1940	
DB	377	AATGTGTGGCCCAACGGGTGGTTCGCAATCTTTTAATCTAGACAAAGAACCCTCGAGAA	318	
QY	1941	ATTCTAGTGCANTATCCAGATTCTGAAAGAGATCCTCATGAAGAAAGCCAGAGTGCCTTTTA	2000	
DB	317	ATTCTAGTGCANTATCCAGATTCTGAAAGAGATCCTCATGAAGAAAGCCAGAGTGCCTTTTA	258	
QY	2001	AAGCAGAAGGCTAAGACCGCAGAAAGCAACCCCTCCAGAAAGAATCTTGTGCCCTCTCTCTTC	2060	
DB	257	AAGCAGAAGGCTAAGACCGCAGAAAGCAACCCCTCCAGAAAGAATCTTGTGCCCTCTCTCTTC	198	
QY	2061	CCACCGAAGAGAGAGACACCCCAACTGTTTTAAACCTCTCTAGGAGGCACAGGAAAGACA	2120	
DB	197	CCACCGAAGAGAGAGACACCCCAACTGTTTTAAACCTCTCTAGGAGGCACAGGAAAGACA	138	
QY	2121	AGTCTTGCAAGACTTACTCAAAATTTGAAGCGAGAGCAAGCAGTCTCAGAGAAAGAAATCTCT	2180	
DB	137	AGTCTTGCAAGACTTACTCAAAATTTGAAGCGAGAGCAAGCAGTCTCAGAGAAAGAAATCTCT	78	
QY	2181	GAGGCGAGGAGGAGAGAGAAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAA	2240	
DB	77	GAGGCGAGGAGGAGAGAGAGAAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAA	18	
QY	2241	CAAAAGAGAAATGAATGAA	2255	
DB	17	CAAAAAAAAAAAAAA	3	

```

RESULT 6
BE287002 881 bp mRNA linear EST 26-OCT-2000
LOCUS 601097229F1 NCI_COAP_Mam5 Mus musculus cDNA clone IMAGE:3496015 5',
DEFINITION BE287002 mRNA sequence.
ACCESSION BE287002
VERSION BE287002.1 GI:9165707
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 881)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8547 row: i column: 08
High quality sequence stop: 774.
Location/Qualifiers
1. .881
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3496015"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mams"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NTH"
ORIGIN
Query Match 14.9%; Score 402.4; DB 10; Length 881;
Best Local Similarity 73.9%; Pred. No. 1.2e-55;
Matches 548; Conservative 0; Mismatches 171; Indels 23; Gaps 2;
QY 1521 TGGAGCTCTCAAGAATGTAGATGAGTCTGATTTGCTTAAGACCCCTACCAACTACGGTC 1580
DB 1 TGGAACTCAAGAATCTCTAGATGAGTCCAACTTGTCTGAGAACCCTCCGACAGCAATG 60
QY 1581 CAGTTAGCCCTCGCCATTCATGTGAACTTCAGCATCATCAGCAAGTCGACTTCTTCAAG 1640
DB 61 CAGTTGCTATTGTCCTTGACATAAACTTCAGTATCATCGACAGGTGGAGTTATTCAAG 120
QY 1641 GGTGTGATACACAGATGATTTATGACATGTTGCTTAAGATTGAATCCGTTCTCTATTG 1700
DB 121 GGCTGTGCACACAGATGATTTATGACCTGCTGCTTAAGATTGAATCCACTATTATTATTA 180
QY 1701 CTTGGTGATCTTCTGCAAAAAGGAGAAATGGCAAGGAAATGTATATCATCAAGCAT 1760
DB 181 CTTGGTGATCTTCTGCAAAAAGGAGAAATGGCAAGGAAATGTATATCATCAAGCAT 240
QY 1761 GGAGAGTCCAAAGTCTTTCGAGCCCTGATGATCTAAAGTCTGGTACTCTGAAGAGCT 1820
DB 241 GGAGAGTCCAAAGTCTTTCGAGCCCTGATGATCTAAAGTCTGGTACTCTGAAGAGCT 300
QY 1821 GGTCGCTGTTGGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCGTCGAACGTCC 1880
DB 301 G-----GCCCTTGCNAAAGGAGGAAATGCCCGACAGCT 339

```

```

QY 1881 AATGTGTCGCCACGGGTTTCCCAATCTTTAACTCTAGACAAAGACCCCTCCAGAA 1940
DB 340 GATGTTGTGGCCACGGATTTCGCCAATCTTTAACTCTGGCAAAAGACTCTCCAAGAA 399
QY 1941 ATTCTAGTGCATTATCCAGATTCTGAAAGGATCTCTCATGAAGAAAGCCAGAGTCTTTTA 2000
DB 400 ATTCTGTCGATTATCCCACTTCTAAAGAGCTCTCATGAAGAAAGCCAAATTCCTTTTA 459
QY 2001 AAGCAGAGGCTAAGACCGCAGACCACTCTCCAGAAAGATCTTGCCTCTCTCTTC 2060
DB 460 AGCCAGAGGGAAGAACCACTCAGGCAATCTCTCAAGACCCAGGACCTGCTTTCTTTTC 519
QY 2061 CCACCGAAGAGAGACACACCCCAAACTGTTTAAAACTCTCTTAGGAGGACAGGAGAAAGCA 2120
DB 520 CCACCAAGAGAGACACACCCCGAATGCTTAAAGTCTCTTAGGACACACAGGAAGGTGG 579
QY 2121 AGTCTTCAGACTACTCAATTTAGCGAGAGCAAGCAGCTCAG--AAGAAAGAAATT 2178
DB 580 ACCTTGGAAAGACTCTTTAAGGAAAGAGAAAAACAACCACTCAGAAATAACGGTGAAA 639
QY 2179 CTGAAGGAGGAGGAGGAAGAAAGAAAGAAATGAAGATAAAACAAAGAAATGAAGATA 2238
DB 640 GTTCCACAGGCAAGAAAAAGAGAGGAGAGAGAAATGAAGACCAAGGACAGAGACTT 699
QY 2239 AACAAAAAGAAATGAAGATAA 2260
DB 700 AGCAGAAAAAGAAAGAAAAA 721
RESULT 7
BX401127 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CSODK009YE13 5-PRIME, mRNA sequence.
ACCESSION BX401127
VERSION BX401127
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7817.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODK009AC07QPi&cluster=7817.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSODK009AC07QPi.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK009YE13"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/clone_lib="HELA"
/notes="First strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 13.5%; Score 363.8; DB 13; Length 1201;

```

Best Local Similarity 60.8%; Pred. No. 1.9e-49;
Matches 611; Conservative 35; Mismatches 353; Indels 6; Gaps 5;

QY 923 AAATGAGCTAAGGAACACTCAGGACTCTTACAAAATTTTCAGTTGGATGTCGATCAAT 982
D 923 AAATGAGCTAAGGAACACTCAGGACTCTTACAAAATTTTCAGTTGGATGTCGATCAAT 982

QY 983 AATACATTTGATTTGCTACCTCTTCTTCTTGGGTTTAAATCCAAATGTTAGAGCAATAG 1042
D 983 AATACATTTGATTTGCTACCTCTTCTTCTTGGGTTTAAATCCAAATGTTAGAGCAATAG 1042

QY 68 CTTGCCCTTGGATTTTCTTATTTGAAAGTCGGTGTGAACCCCTCTCCGCTGTCMCCG 127
D 68 CTTGCCCTTGGATTTTCTTATTTGAAAGTCGGTGTGAACCCCTCTCCGCTGTCMCCG 127

QY 1043 GATGTTAA--GTACACTTCAATTTTGAATTTTAAATCATCACCTAGAGTTAATGGAC 1100
D 1043 GATGTTAA--GTACACTTCAATTTTGAATTTTAAATCATCACCTAGAGTTAATGGAC 1100

QY 128 CTGTTTAAATGATCATCGCTTCTTCCGTTTAAACGCCCTCGGAATCATCTCAGC 187
D 128 CTGTTTAAATGATCATCGCTTCTTCCGTTTAAACGCCCTCGGAATCATCTCAGC 187

QY 1101 AAAGCATATATCATAGAGTTATTCGAACAACTGGATATCTGCTGTTTATTTCTGCACAT 1160
D 1101 AAAGCATATATCATAGAGTTATTCGAACAACTGGATATCTGCTGTTTATTTCTGCACAT 1160

QY 188 AAAGCCTACGTGTACAGGTCATCAGGAYCACAGTACCTTCTTACAGCCTGCAATTG 247
D 188 AAAGCCTACGTGTACAGGTCATCAGGAYCACAGTACCTTCTTACAGCCTGCAATTG 247

QY 1161 AATGCTGTGTTTATCTAGGCTTCAAACTATGAAGATTTGCACTACTAGATGGTG 1220
D 1161 AATGCTGTGTTTATCTAGGCTTCAAACTATGAAGATTTGCACTACTAGATGGTG 1220

QY 248 AATTCCTGCTTTTATCTGGAATCGGCTTATCAGGCTTCCGCTTCACTCAGCTGGTT 307
D 248 AATTCCTGCTTTTATCTGGAATCGGCTTATCAGGCTTCCGCTTCACTCAGCTGGTT 307

QY 1221 TATGATGGGAGGAAACAGATCTGAGATGTTTATTTGGGAGTTGCAATTTAAT 1280
D 1221 TATGATGGGAGGAAACAGATCTGAGATGTTTATTTGGGAGTTGCAATTTAAT 1280

QY 308 TACGATGGCTGGGAAACAGTATATTCGCTGTACTTCTGCTGTGAACATCCTATC 367
D 308 TACGATGGCTGGGAAACAGTATATTCGCTGTACTTCTGCTGTGAACATCCTATC 367

QY 1281 ACCATGCTGGCTTCCAGACCAACAACTTATTTGAAATGTTTTCACCTTGAAT 1340
D 1281 ACCATGCTGGCTTCCAGACCAACAACTTATTTGAAATGTTTTCACCTTGAAT 1340

QY 368 ATCATCGGGGGCTGCTCCGACCCCAAGAYACTCTTTGAAATGTTCTCCAGCTGYTGAAT 427
D 368 ATCATCGGGGGCTGCTCCGACCCCAAGAYACTCTTTGAAATGTTCTCCAGCTGYTGAAT 427

QY 1341 TTTTCTGAGGTTTGTCTTCTCCAGTTTAAATTTGGTGTGAGATGAGATGGA 1400
D 1341 TTTTCTGAGGTTTGTCTTCTCCAGTTTAAATTTGGTGTGAGATGAGATGGA 1400

QY 428 TATTTTCAAGGGCTGCTTCTTCTGCTGTGATTTGACAGATGAGATGTTGAGG 487
D 428 TATTTTCAAGGGCTGCTTCTTCTGCTGTGATTTGACAGATGAGATGTTGAGG 487

QY 1401 CGAGTACAGCCATCAGAACTACTTTCGGCTTGGATGATGATGATGATGATGATGATG 1460
D 1401 CGAGTACAGCCATCAGAACTACTTTCGGCTTGGATGATGATGATGATGATGATGATG 1460

QY 488 GCGGCAACG-CAGACAGCTACTTACCGAGCTGCTGATGAGACAGCAGGTGAAGTACATG 546
D 488 GCGGCAACG-CAGACAGCTACTTACCGAGCTGCTGATGAGACAGCAGGTGAAGTACATG 546

QY 1461 AACATTTACTCCATTTCTTAACTTTGTGCAAAAGGAGTTGCGACTTGGTATGATATACA 1520
D 1461 AACATTTACTCCATTTCTTAACTTTGTGCAAAAGGAGTTGCGACTTGGTATGATATACA 1520

QY 547 AATTTTCAAGATCCCCAAGTCGGTGCAGAACGAGTCAAGACCTGGTGAAGATACACC 606
D 547 AATTTTCAAGATCCCCAAGTCGGTGCAGAACGAGTCAAGACCTGGTGAAGATACACC 606

QY 1521 TGGGACTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1580
D 1521 TGGGACTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1580

QY 607 TGGCCTCGAAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 666
D 607 TGGCCTCGAAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 666

QY 1581 CAGTTAGCCCTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1640
D 1581 CAGTTAGCCCTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1640

QY 667 CGGCTGGACCTCGCCATCGACATGAATCAACATCGTTAGCAAGTCCGACTCTTTCAG 726
D 667 CGGCTGGACCTCGCCATCGACATGAATCAACATCGTTAGCAAGTCCGACTCTTTCAG 726

QY 1641 GGTGTGATACACAGATGATTTATGATGATGATGATGATGATGATGATGATGATGATG 1700
D 1641 GGTGTGATACACAGATGATTTATGATGATGATGATGATGATGATGATGATGATGATG 1700

QY 727 GCTGTGACCGGAGATGATCTTTGATGATGATGATGATGATGATGATGATGATGATG 786
D 727 GCTGTGACCGGAGATGATCTTTGATGATGATGATGATGATGATGATGATGATGATG 786

QY 1701 COTGTGACTTTGTCTGCAA-AAAGGAGAAATTTGCAAGGAAATGATATCATCAAGCA 1759
D 1701 COTGTGACTTTGTCTGCAA-AAAGGAGAAATTTGCAAGGAAATGATATCATCAAGCA 1759

QY 787 CCCAACGACTATGTGCAAGAAVGGSSAGATCGGCGGTGAGATGATATCATCAAGCA 846
D 787 CCCAACGACTATGTGCAAGAAVGGSSAGATCGGCGGTGAGATGATATCATCAAGCA 846

QY 1760 TGGAGATCCAGTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGATG 1819
D 1760 TGGAGATCCAGTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGATG 1819

QY 847 AGGCAAGTCAGGCTTGGGCGGCTGATGAGAAATCTGCTGTGTGA-GCTKCAAS 905
D 847 AGGCAAGTCAGGCTTGGGCGGCTGATGAGAAATCTGCTGTGTGA-GCTKCAAS 905

QY 1820 TGGTTCGCTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAAACCGTCCGAATCG 1879
D 1820 TGGTTCGCTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAAACCGTCCGAATCG 1879

QY 906 KSSATYTGTTTGSAGAAWAAGCTTCTGCTGCTGTTTGGGGCGGCA-DGGGCGCAGCC 964
D 906 KSSATYTGTTTGSAGAAWAAGCTTCTGCTGCTGTTTGGGGCGGCA-DGGGCGCAGCC 964

QY 1880 CAATGTGTGCCCAAGGTTTGCATCTTTTAACTCTAGACAA 1924
D 1880 CAATGTGTGCCCAAGGTTTGCATCTTTTAACTCTAGACAA 1924

QY 965 CAAGTGTGSSSSMGGGTTTACMANCTCTTATCTTATCTTATCTTATCTTATCTTATCT 1009
D 965 CAAGTGTGSSSSMGGGTTTACMANCTCTTATCTTATCTTATCTTATCTTATCTTATCT 1009

RESULT 8

BI827605
LOCUS 603073571F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5165752 5',
DEFINITION mRNA sequence.
ACCESSION BI827605
VERSION BI827605.1 GI:15939142
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 832)
AUTHORS Mammalia; Eukarya; Chordata; Vertebrata; Euteleostomi;
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM1411 Row: m column: 17
High quality sequence stop: 817.
Location/Qualifiers
1..832
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5165752"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen) Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 12.1%; Score 328.4; DB 12; Length 832;
Best Local Similarity 99.4%; Pred. No. 1.2e-43;
Matches 340; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 2345 TGCAGTGGAGGAAGAACCCCACTC-AGTTAGAGGACAGTTTACCAGAGGACTTCTC 2403
D 1 TGCAGTGGAGGAAGAACCCCACTCAGTTAGAGGACAGTTTACCAGAGGACTTCTC 60
QY 2404 GTCATCACTCATTTATCAGCATGGCTCTCTCTGCTGAGGCGGAGAGAGTTCTTACTA 2463
D 61 GTCATCACTCATTTATCAGCATGGCTCTCTCTGCTGAGGCGGAGAGAGTTCTTACTA 120
QY 2464 TTGAAGTCAAGAAAGCTAAGCAATAATCTTTGATTTCTTTAGATGTATAGCT 2523
D 121 TTGAAGTCAAGAAAGCTAAGCAATAATCTTTGATTTCTTTAGATGTATAGCT 180
QY 2524 AGTTCCCAAGTGTATTGATCTAGGATTTAACTTAAATTAACGAGGGAACGACATGC 2583
D 181 AGTTCCCAAGTGTATTGATCTAGGATTTAACTTAAATTAACGAGGGAACGACATGC 240
QY 2584 TGGACCCCTTGAGAAACGAAAGCAATCCCTAGCTTAGTTCTTAGACTTATCTGAGAG 2643
D 241 TGGACCCCTTGAGAAACGAAAGCAATCCCTAGCTTAGTTCTTAGACTTATCTGAGAG 300
QY 2644 TGTGATTTTCATGCAAGTGTGTAATAAGAGATTATTAAGGCA 2685
D 301 TGTGATTTTCATGCAAGTGTGTAATAAGAGATTATTAAGGCA 342

```

RESULT 9
AA069559
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
and Marra, M.

TITLE
Generation and analysis of 280,000 human expressed sequence tags

JOURNAL
Genome Res. 6 (9), 807-828 (1996)
MEDLINE
97044478
PubMed
889549
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 874 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 382.
Location/Qualifiers
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1290991"
/db_xref="taxon:9606"
/clone="IMAGE:382734"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/notes="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site.1: Not I; Site.2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTTTTTTTTTTTTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library constructed by Bento Soares
and M.Patima Bonaldo."

FEATURES
source
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1290991"
/db_xref="taxon:9606"
/clone="IMAGE:382734"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/notes="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site.1: Not I; Site.2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTTTTTTTTTTTTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library constructed by Bento Soares
and M.Patima Bonaldo."

ORIGIN
Query Match 11.9%; Score 320.8; DB 9; Length 468;
Best Local Similarity 97.9%; Pred. No. 2.8e-42;
Matches 325; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 81 AAGTCAACAGGTGAAGCGCTATAGGAGAGAACAAATGAGAAATGAACAAAGTTCTCGCG 140
DB 2 AAGTCAACAGGTGAAGCGCTATAGGAGAGAACAAATGAGAAATGAACAAAGTTCTCGCG 61
QY 141 AATGAAGAGCGTCTCAACCAAGTAATCAGTCTCAGCAACACACAGCAGGAGAAAC 200
DB 62 AATGAAGAGCGTCTCAACCAAGTAATCAGTCTCAGCAACACACAGCAGGAGAAAC 121
QY 201 AAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCCTGAAGAGCCACAC 260
DB 122 AAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCCTGAAGAGCCAC 181

```

```

QY 261 ACCAACAATACAGACAAACTCTCCAGAAATATTCCTCTGGAGATCTGACCAACACCT 320
DB 182 ACCAACAATACAGACAAACTCTCCAGAAATATTCCTCTGGAGATCTGACCAACACCT 241
QY 321 GACCTCAAATGCAGCAGACCAACTGGAACAGTCCAGAGCAGAGGAAATGGACCCC 380
DB 242 GACCTCAAATGCAGCAGACCAACTGGAACAGTCCAGAGCAGAGGAAATGGACCCC 301
QY 381 GGGAAAGAGGTTCCTCAACAGCCCAACAAACAA 412
DB 302 GGGAAAGAGGTTCCTCAACAGCCCTAGAA 333

H53423 445 bp mRNA linear EST 20-SEP-1995
Yc86a09.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:231160 5', mRNA sequence.
H53423
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 445)
AUTHORS
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
and Marra, M.
TITLE
Generation and analysis of 280,000 human expressed sequence tags
JOURNAL
Genome Res. 6 (9), 807-828 (1996)
MEDLINE
97044478
PubMed
889549
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 903
High quality sequence stop: 302
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 903 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 302.
Location/Qualifiers
1..445
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3861151"
/db_xref="taxon:9606"
/clone="IMAGE:231160"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/notes="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site.1: Not I; Site.2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTTTTTTTTTTTTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library constructed by Bento Soares
and M.Patima Bonaldo."

ORIGIN
Query Match 11.7%; Score 317; DB 14; Length 445;
Best Local Similarity 91.1%; Pred. No. 1.2e-41;

```

	Matches	349;	Conservative	0;	Mismatches	27;	Indels	7;	Gaps	1;
QY	25	CATAAATACAGAGGGTTTTCAGAACACACCTCAGAGAGATGTTTAAATCGCTGACAAAAG	84							
Db	1	CATAAATACAGAGGGTTTTCAGAACACACCTCAGAGAGATGTTTAAATCGCTGACAAAAG	60							
QY	85	TCAACAAGGTGAAGCCCTATATAGGAGAGAACAAATGAGAAATGAACAAAGTTCCTGTCGGAAATG	144							
Db	61	TCAACAAGGTGAAGCCCTATATAGGAGAGAACAAATGAGAAATGAACAAAGTTCCTGTCGGAAATG	120							
QY	145	AAGAAGGCTCTCACCCCAAGTAATCAGTCTCAGCAAAACACAGCACAGGAAGAAAAACAAG	204							
Db	121	AAGAAGGCTCTCACCCCAAGTAATCAGTCTCAGCAAAACACAGCACAGGAAGAAAAACAAG	180							
QY	205	GTGAAGAGAAAATCTCTCAAAACCAAGTCAACTCCAGTCAAGTCTGAAGAGCCACACACCA	264							
Db	181	GTGAAGAGAAAATCTCTCAAAACCAAGTCAACTCCAGTCAAGTCTGAAGAGCCACACACCA	240							
QY	265	ACATCAGAGCAAACTCTCCAGGAAAATTCCTCTGGAGATCTCACCACAAAACCCCTGACC	324							
Db	241	ACATCAGAGCAAACTCTCCAGGAAAATTCCTCTGGAGATCTCACCACAAAACCCCTGACC	300							
QY	325	CTCAAAATCAGACAGAAACCAACTCGAAACAGTCCAGAGCAGGAAGAAAATGGA-----C	377							
Db	301	CTCAAAATCAGACAGAAACCAACTCGGAACAGTTCGCCAGAGCAGGAAGGAATGGGACC	360							
QY	378	CCCGGGAAAAGAGTCCAAACAG	400							
Db	361	CGGGGNAAGGAAGGTNCAAAACAG	383							

RESULT 11
BQ068992
LOCUS BQ068992 978 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6740166 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802872
5', mRNA sequence.

FEATURES source

RESULT 12	AU137778	694 bp	mrna	linear	EST 02-AUG-2002
LOCUS	AU137778		clone		
DEFINITION	AU137778 PLACE1 Homo sapiens cDNA clone PLACE1007225 5', mRNA sequence.				
ACCESSION	AU137778				
VERSION	AU137778.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 694)				
AUTHORS	Ora, T., Nishikawa T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakanatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.				
TITLE	HRI human cDNA project				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takao Isogai				

Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

source

1. .694
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="PLACE1007225"
 /tissue_type="placenta"
 /clone_lib="PLACE1"
 /note="Vector: pME189FL3"

ORIGIN

Query Match 11.2%; Score 301.4; DB 9; Length 694;
 Best Local Similarity 66.3%; Pred. No. 3.2e-39;
 Matches 445; Conservative 0; Mismatches 225; Indels 1; Gaps 1;
 QY 1111 TCTACAGAGTTATTCGAACAACCTGGATCTTCTGCTTTTATTCACATTAATGCTGTG 1170
 DB 20 TCTGAGGGTATCAGGACCAAGCTTCTCTACAGCTGCAATTTGAATTCCTGTC 79
 QY 1171 TTTATTATCGGCTTCAAACTATGAAGAAATGGCACTTACAGATGGGTGTATGATGGG 1230
 DB 80 TTTATTATCGGCTATCGGCTTATCAGGCTCCGCTCCACTCACTGGTGTACGATGGG 139
 QY 1231 AAGGAACAGATCTGAGATGTTATTATTGGCAGTTCGAACTTATACCAATGGTG 1290
 DB 140 TGGGAACAGTTATTCGCTGTGTACTCTTGTGTGAAGACCTCATCACCATCGGG 199
 QY 1291 GCCTTCCAGAACCAAACTTTATTGAAATGTTTTTCACTCTTGAATTTTTTTCTG 1350
 DB 200 GGCTGCTGACCCCAAGACACTTTTGAATTTGCTTCCAGCTCTGAATTTTCAAG 259
 QY 1351 GAGTTTGTGTTCTCCAGTTAATTTGTGATGAGATGATGATGGAGCTACAG 1410
 DB 260 GCGTCTTGTCTTCTGTGATGATCGACAGATGAGATGTGTAGGGGCGGCCACCG 319
 QY 1411 CCAATCAGAACTACTTCCGCGCTGATGATGACACCATTCCTCATGAACAATTA 1470
 DB 320 CGGACAGACCTACTACCGAGCTGCATGACAGACAGGTGAAGTATTTCTACA 379
 QY 1471 CCATTCCTAACTTGTGCAAAAGCGAGTTGGACTTGTATGATATACATGGGACTTC 1530
 DB 380 AGATCCCCAAGTCCGTGCGAGAACCGCTCAAGACCTGGTACGATACACCTGGCACTCGC 439
 QY 1531 AAAGATCTAGATGAGTCTGATTTGCTTAAGACCTTACCACTACCGTCCAGTTAGCCC 1590
 DB 440 AAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 499
 QY 1591 TCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1650
 DB 500 TCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 559
 QY 1651 CACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710
 DB 560 GGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
 QY 1711 TTGTTCTGAAA - AAGGGAGAAATTTGGCAAGAAATTTATATCATCAAGCATGAGAGATC 1769
 DB 620 ATGTGTGCAAGAGAGGGGAAATCGGCGTGTGATGATGATGATGATGATGATGATGATGAT 679
 QY 1770 CAAGTTCTTG 1780
 DB 680 CAAGTCTNTGG 690

RESULT 13

BX104558

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX104558 741 bp mRNA linear EST 06-FEB-2003
 BX104558 Soares pineal gland 3NBHPC Homo sapiens cDNA clone
 IMAGE:384252, mRNA sequence.
 BX104558
 BX104558.1 GI:27832995
 EST.
 Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 741)
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radelof, U., Schneider, D. and Korn, B.
 Human Unigeneset - RZPD3
 Unpublished (2003)
 Contact: Ina Rolfes
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGP998P13890.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No. 972)
 http://www.rzpd.de/ClonesCards/cgi-
 bin/showLib.pl.cgi/responder?libNo=972 Contact: Ina Rolfes
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTCACAGAGAAACAGCTATGAC.
 Location/Qualifiers
 1. .741
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGP998P13890 ; IMAGE:384252"
 /tissue_type="brain, pineal gland"
 /dev_stage="adults (ages 18, 20, 48)"
 /lab_host="DH10B"
 /clone_lib="Soares pineal gland 3NBHPC"
 /note="1st strand cDNA (prepared from post mortem tissue)
 was primed with a Not I - oligo(dT) primer [5',
 TGTTACCAATCTGAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to EcoRI adaptors
 5'-AATTCGGACGAGG-3' and 5'-CCTCGTGGCG-3' (Pharmacia),
 digested with NotI and cloned into the NotI and EcoRI
 sites of the pT73D-Paci vector. Library went through one
 round of normalization, to Cot38. Library constructed by
 Bento Soares and M. Fatima Bonaldo"

FEATURES

source

1. .741
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGP998P13890 ; IMAGE:384252"
 /tissue_type="brain, pineal gland"
 /dev_stage="adults (ages 18, 20, 48)"
 /lab_host="DH10B"
 /clone_lib="Soares pineal gland 3NBHPC"
 /note="1st strand cDNA (prepared from post mortem tissue)
 was primed with a Not I - oligo(dT) primer [5',
 TGTTACCAATCTGAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to EcoRI adaptors
 5'-AATTCGGACGAGG-3' and 5'-CCTCGTGGCG-3' (Pharmacia),
 digested with NotI and cloned into the NotI and EcoRI
 sites of the pT73D-Paci vector. Library went through one
 round of normalization, to Cot38. Library constructed by
 Bento Soares and M. Fatima Bonaldo"

ORIGIN

Query Match 10.6%; Score 286.8; DB 13; Length 741;
 Best Local Similarity 97.7%; Pred. No. 7.2e-37;
 Matches 291; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 QY 115 ATGAGAATGAACAAGTTCTCGTGGATGAAGAGGCTCTCACCCAGTAAATCAGTCTC 174
 DB 1 ATGAGAATGAACAAGTTCTCGTGGATGAAGAGGCTCTCACCCAGTAAATCAGTCTC 60
 QY 175 AGCAACACACAGCAGGAGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAA 234
 DB 61 AGCAACACACAGCAGGAGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAA 120
 QY 235 CTCAGTCACTCTGAGAGCCACACACCAATACATACAGCAAACTCTCCAGAAATTT 294
 DB 121 CTCAGTCACTCTGAGAGCCACACACCAATACATACAGCAAACTCTCCAGAAATTT 180
 QY 295 CCTCTGGAGATCTGACCAAAACCTCGACCTCAAAATGCGAGAGAACCACTGGACAG 354

```

Db      181 CCTCTGAGATCTGACCACAAACCCCTGACCCCTCAAAATGCAGCAGAACCAACTGGAACAG 240
QY      355 TGCAGAGCAGAGAAATGGACCCCGGGAAGAAGTCCAAACACGCCACCAAAACAA 412
Db      241 TGCAGAGCAGAGAAATGGACCCCGGGAAGAAGTCCAAACACGTTGACCCCTAGAA 298

RESULT 14
BI736222
LOCUS   60359912F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5367194 5',
DEFINITION mRNA sequence.
ACCESSION BI736222
VERSION   BI736222.1 GI:15713235
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 738)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
        Email: cgaps-remail.nih.gov
        Tissue Procurement: The Cepko Laboratory
        CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: LLAM11934 row: g column: 03
        High quality sequence stop: 736.

FEATURES             source
    source
        1..738
            Location/Qualifiers
                1..738
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:5367194"
                    /tissue_type="retina"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_94"
                    note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
                    Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
                    Average insert size 3.3 kb. Library enriched for
                    full-length clones and constructed by Life Technologies.
                    Note: this is a NIH_MGC Library."

ORIGIN
Query Match      10.4%; Score 280.8; DB 12; Length 738;
Best Local Similarity 63.0%; Pred. No. 6.7e-36;
Matches 466; Conservative 0; Mismatches 272; Indels 2; Gaps 2;

QY      810 ATACACTACTGGCTTATTCGGACATCATATGTGATATCATCTACCTTTATGATGCTA 869
Db      1 ATCCACTTCTGGCTCTCATGATTAATCTTGTGGACTTCATCTACCTCTCGACATCACC 60
QY      870 TTATPCCAGCCAGACTCCAGTTTGTAAAGAGAGAGACATAATAGTGGATCAATGAG 929
Db      61 GTGTTCCAGATGCGGCTGCAG-TTGTCAAAGGCGGGGACATCATTTACAGACAAGAGGAG 119
QY      930 CTAAGGAACACTCAGACACTTCTACAAAATTTTCAGTTGGATGTGGCATCAATAATACCA 989
Db      120 ATGCGATAATAACTACTTGAACCTTGGCATCAACCTCTCCCTGGCTGCCCTGCTGCCC 179
QY      990 TTGTGATTTGTACTCTCTTTTGGGTTTATCCAAATGTTTAGAGCAAAATAGGATGTTA 1049
Db      180 TTGGACTTCTCTACTTGAACCTTGGCATCAACCTCTCCCTGGCTGCCCTGCTGCCC 239
QY      1050 AAGTACACTTCAATTTTGAATTTTATCATCACTAGAGTCTATAATGGACAAAGCATAT 1109
Db      240 AAGTACATGGCCCTTCTTTGAGTTTAAATACCGCCTGGGAAGCCATCTCAGCAAAAGCCTAC 299

```

```

QY      1110 ATCTACAGAGTATTTCGAACAACCTGGATACTTGTGTTTATTTCGCAATTAAATGCGCTGT 1169
Db      300 GTTTACAGAGTCATCAGGACCAACGGCTTACCTGCTGTACAGCTGCACTCAACTCCTTGC 359
QY      1170 GTTTATTACTGGCTTCAAACTATGAAGGAATTCGCACTACTAGATGGTGTATGATGGG 1229
Db      360 CTTTACTACTGGCATCAGCCT-TCCAGGCATCGGCTCCACTCTCTGGGTTTACACGGA 418
QY      1230 GAAGGAAAACGAGTATCTCAGATGTTATTATTGGGCAGTTCGAACCTTTAAATTAACCATTTGGT 1289
Db      419 GTGGGGAACAGTTATTTCGATGCTACTTACTGGGCTGTGAAAACCTCATCACCATCGGA 478
QY      1290 GGCCTTCCAGAACCAACAACTTTATTGAAATGTTTTCACCTCTGAAATTTTCTTCT 1349
Db      479 GGACTGCCCGACCCCGACAGCGCTCTTTGAGATGTTCTTCCAGCTGCTGAATTTTACC 538
QY      1350 GGAGTTTTTGTCTCTCCAGTTTAAATGTCAGATGAGAGATGTGATTGGAGCAGCTACA 1409
Db      539 GGGGTTCTTTGCTTCTCTGTGATGATTCGACAGATGAGAGATGTGTTGGGGCCGCCACA 598
QY      1410 GCCAATCAGAACTACTTCCGGCCCTGCATGGATGACACACCATTCCTACATGAACAATTAC 1469
Db      599 GCGGGGCAGACCTACTACCGCAGCTGCATGGACACACAGTGAAGTACATGAACCTTCTAC 658
QY      1470 TCCATTCCCTAAACTTGTGCAAAAGCGAGTTCGGACTTGTGATGAATATACATGGGACTCT 1529
Db      659 AAGATCCCCAGGTCTGTGCAGAACCGTGTCAAGACCTGGTATGAGTACACCTGGCATTCG 718
QY      1530 CAAAGAATGCTAGATGAGTC 1549
Db      719 CAAGGCATGCTGATGAGTC 738

```

```

RESULT 15
AV726367      758 bp      mRNA      linear      EST 16-OCT-2000
LOCUS        AV726367      HTC Homo sapiens cDNA clone HTCCDC01 5', mRNA sequence.
DEFINITION   AV726367
ACCESSION    AV726367
VERSION      AV726367.1 GI:10832695
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 758)
AUTHORS      Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
            Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
            Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
            Chen, J., Chen, Z. and Han, Z.
            Homo sapiens cDNA HTC clones
            Unpublished (2000)
            Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919 (ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.

FEATURES             source
    source
        1..758
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="HTCCDC01"
            /tissue_type="Hypothalamus"
            /dev_stage="Adult"
            /lab_host="SOLR"
            /clone_lib="HTC"
            /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
            XhoI"

```

Query Match 10.4%; Score 280.4; DB 9; Length 758;
Best Local Similarity 99.8%; Pred. No. 7.7e-36;
Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2404 GTCAATCACTCATTATCAGCATGGCTCTCTGCTGAGGGCGGAGAGAGGTTCTTACTA 2463
|||
Db 1 GTCAATCACTCATTATCAGCATGGCTCTCTGCTGAGGGCGGAGAGAGGTTCTTACTA 60
|||

QY 2464 TTGAAGTCAAGAAAGGCTAAGCAATAAATGTTTGATTATCTTTAGATGATATAGCT 2523
|||
Db 61 TTGAAGTCAAGAAAGGCTAAGCAATAAATGTTTGATTATCTTTAGATGATATAGCT 120
|||

QY 2524 AGTTCCCAAAGTGATTGTACCTAGGATTGTTAAATTAACGAGGGGAAACGACATGC 2583
|||
Db 121 AGTTCCCAAAGTGATTGTACCTAGGATTGTTAAATTAACGAGGGGAAACGACATGC 180
|||

QY 2584 TGGGACCCCTTGAGAAACGAAAGGCAATCCCTAGCTTAGTTTCTAGGACTTATCTGAGAG 2643
|||
Db 181 TGGGACCCCTTGAGAAACGAAAGGCAATCCCTAGCTTAGTTTCTAGGACTTATCTGAGAG 240
|||

QY 2644 TGTGATTTTCATGCAGTGGTAATARGAGATTATTAAAGCAA 2685
|||
Db 241 TGTGATTTTCATGCAGTGGTAATARGAGATTATTAAAGCCA 282
|||

Search completed: June 22, 2004, 04:03:28
Job time : 6766.81 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:22:44 ; Search time 183.254 Seconds
(without alignments)
8185.526 Million cell updates/sec

Title: US-09-855-828-2
Perfect score: 2703
Sequence: 1 cattctctacctaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/6CTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	100.8	3.7	7218	1	US-08-232-463-14
2	85.6	3.2	2223	1	US-08-257-073-4
C 3	78.8	2.9	929	4	US-09-671-317-14
C 4	72.8	2.7	1001	4	US-09-671-317-439
C 5	66.6	2.5	396	4	US-09-640-173-53
C 6	66.6	2.5	396	4	US-09-713-550-53
7	66.2	2.4	2394	4	US-08-800-729-33
8	65.6	2.4	1696	4	US-09-835-811-1
9	65.6	2.4	2447	2	US-09-014-969-14
10	64.8	2.4	43795	3	US-08-742-185-101
11	64.2	2.4	240	1	US-08-628-417-6
12	64	2.4	1447	4	US-09-443-041A-27
13	63	2.3	674	4	US-09-620-405B-465
14	63	2.3	674	4	US-09-433-826B-465
15	63	2.3	674	4	US-09-604-287A-465
16	63	2.3	674	4	US-09-834-759-465
17	62.8	2.3	1051	3	US-08-245-041-10
C 18	62.6	2.3	118067	4	US-09-497-855A-32
C 19	62.2	2.3	16442	3	US-08-781-891-208
C 20	62.2	2.3	16442	4	US-09-618-166-208
21	61.6	2.3	249	4	US-08-621-976-1322
22	61.6	2.3	2608	4	US-09-904-615-16
23	61.6	2.3	3211	2	US-08-574-959A-8
24	61.6	2.3	3211	3	US-09-357-014-8
25	61.6	2.3	3901	2	US-08-574-959A-6
26	61.6	2.3	3901	3	US-09-357-014-6
27	61.4	2.3	282	3	US-09-461-697-205

Query Match 3.7%; Score 100.8; DB 1; Length 7218;

ALIGNMENTS

RESULT 1

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ59pT-F1s
; US-08-232-463-14

Sequence 203, App
Sequence 133, App
Sequence 191, App
Sequence 189, App
Sequence 187, App
Sequence 185, App
Sequence 184, App
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 1324, Ap
Sequence 47, Appli
Sequence 1, Appli
Sequence 207, App
Sequence 44, Appli
Sequence 2, Appli

Best Local Similarity 12.8%; Pred. No. 1.9e-15;
Matches 57; Conservative 231; Mismatches 158; Indels 0; Gaps 0;
QY 2066 GAAAGAGAGACACCAAACTCTTTAAACTCTCTAGGAGGACAGGAAAGCAAGTCT 2125
DB 1381 RRR 1322
QY 2126 TCAAGACTACTCAAAATGAGCGAGACCAAGCTCAGAGAAAGAAAATTCGAAGG 2185
DB 1321 RRR 1262
QY 2186 AGGAGAGAGAGAGCAAGAAAGAAATGAAGATAACAAAGAAATGAAGATAACAAA 2245
DB 1261 RRR 1202
QY 2246 AGAAATGAAGATAAGGAAAGAAATGAAGATAAGAAAGAGAGAGAGAGAGAGAG 2305
DB 1201 RRR 1142
QY 2306 GAAGCACTGACAGACCTGAATGTACAGAGTCTTTCAGTGGAGAGAGAGAGAG 2365
DB 1141 RRR 1082
QY 2366 CTCAGTTAGAGGACAGTTTACCCAGAGGACTTCTCGTCAATCACTCATTTATCAGCAT 2425
DB 1081 RRR 1022
QY 2426 CGCTCTTCTGCTGAGGCGGAGAGAGGTTCTTACTATTGAAGTAAAGAGAGGCTAA 2485
DB 1021 TGAGCGTATGGCAAGCAAGGAAATAGTTATAGTACCGCACTCGATGGACATTTC 962
QY 2486 GCAATAAATGTTGATTATCTTTAGA 2511
DB 961 ACCTAACCGTTTAAATAATTTTGA 936

RESULT 2

US-08-257-073-4
; Sequence 4, Application US/08257073
; Patent No. 576597
; GENERAL INFORMATION:
; APPLICANT: Faolletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425086 CURTMS
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-073-4
Query Match 3.2%; Score 85.6; DB 1; Length 2223;
Best Local Similarity 68.6%; Pred. No. 7.4e-12;
Matches 118; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 2150 AGAGCAGCAGCTCAGAGAAAGAAAATTCCTGAGGAGGAGAGAGAGAGAGAGAG 2209
DB 2016 AAATAGGAG 2075
QY 2210 TGAAGATAACAAAGAAAGAAATGAAGATAACAAAGAAAGAAATGAAGATAACAA 2269
DB 2076 AG 2135
QY 2270 AAATAGAGATAAGATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2321
DB 2136 AGAAG 2187

RESULT 3

US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.misl, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 634..652


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI94-07A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-742-185-101

Query Match      2.4%; Score 64.8; DB 3; Length 43795;
Best Local Similarity 63.5%; Pred.No. 6.1e-06;
Matches 99; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY    2149   GAGAGCAACGACTCTGAGAAGAAGAAATTTGAAGGAGGAGCAGGAAGAAAAGAAA 2208
Db     38894   GAGATTGAGAAGAAAAGAAAAAAGAAAGAAAGAGAGAGGAAGCGGGAAGAGAGAGA 38953

QY    2209   ATGACGATATAACAAGAAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAAGGAAAAAG 2268
Db     38954   AGGACGGAGAGGAGNAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39013

QY    2269   AAAATCAAGATAAAGATAAAGGAAGAGCCGAGAG 2304
Db     39014   AAGAGAGGAGGAAGAAGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39049

RESULT 11
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESSEE: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid

```


Db 552 AAA 611
Qy 2230 ATCAAGATTAACAAAAGAGATGTAGATAAAGGAAAGAAATGAAGATAAAGATAAG 2289
Db 612 AAA 671
Qy 2290 GAA 2292
Db 672 AAA 674

RESULT 15
US-09-604-287A-465
; Sequence 465, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 465
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-465

Query Match 2.3%; Score 63; DB 4; Length 674;
Best Local Similarity 59.0%; Pred. No; 2.2e-06;
Matches 108; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
Qy 2110 CAGGAAAGCAAGTCTTGCAAGACTACTCAAATTGAAGCGAGAGCGAGCTCAGAAGA 2169
Db 492 CAGCAAAAGGAGACCTAGGAAGATCGCATGGGAGAAAAGATGACTCAGTTAAGGCAA 551
Qy 2170 AAGAAATTTCTGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2229
Db 552 AAA 611
Qy 2230 ATGAAGATAAACAAAAAGAAAATGAGATTAAGGAAAGAAAATGAAGATAAAGATAAG 2289
Db 612 AAA 671
Qy 2290 GAA 2292
Db 672 AAA 674

Search completed: June 22, 2004, 04:09:24
Job time : 190.254 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 00:29:50 ; Search time 1106.37 Seconds
(without alignments)
11192.162 Million cell updates/sec

Title: US-09-855-828-2

Perfect score: 2703
Sequence: 1 cattctctacttaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577.4	21.4	2607	16	US-10-189-507-3
2	577.4	21.4	4382	16	US-10-159-563-147
3	306	11.3	680	13	US-10-027-632-204539
4	306	11.3	680	16	US-10-027-632-204539
5	176.4	6.5	2500	13	US-10-342-887-427
6	176.4	6.5	2500	13	US-10-172-118-427
7	133.2	4.9	3027	15	US-10-295-573-1
8	132.8	4.9	2085	15	US-10-345-680-27
9	132.8	4.9	1995	15	US-10-087-217-1
10	131.6	4.9	1995	15	US-10-087-217-1
11	131.6	4.9	1995	15	US-10-087-217-5
12	131.6	4.9	3027	15	US-10-295-573-2
13	131.6	4.9	3027	15	US-10-295-573-4
14	129	4.8	526	9	US-09-864-761-12975

15	128.4	4.8	1995	15	US-10-087-217-3	Sequence 3, Appli
16	128.4	4.8	1995	15	US-10-087-217-7	Sequence 7, Appli
17	128	4.7	2677	15	US-10-295-573-3	Sequence 3, Appli
18	127	4.7	127	9	US-09-864-761-29538	Sequence 29538, A
19	111.2	4.1	1995	14	US-10-034-843-1	Sequence 1, Appli
20	111.2	4.1	1995	14	US-10-034-843-1	Sequence 1, Appli
21	111.2	4.1	1995	15	US-10-168-651-34	Sequence 34, Appli
22	111.2	4.1	1995	16	US-10-189-507-1	Sequence 1, Appli
23	111.2	4.1	2111	15	US-10-114-153-17	Sequence 17, Appli
24	111.2	4.1	2190	15	US-10-029-677-23	Sequence 23, Appli
25	111.2	4.1	12017	9	US-09-735-927-3	Sequence 3, Appli
26	109.6	4.1	1995	16	US-10-189-507-4	Sequence 4, Appli
27	109.6	4.1	2186	15	US-10-029-677-1	Sequence 1, Appli
28	84	3.1	31124	13	US-10-087-192-463	Sequence 463, App
29	81	3.0	625	13	US-10-027-632-179350	Sequence 179350,
30	81	3.0	625	16	US-10-027-632-179350	Sequence 179350,
31	80	3.0	2332	15	US-10-087-464-45	Sequence 45, Appli
32	79.6	2.9	305	9	US-09-864-761-19262	Sequence 19262, A
33	79.6	2.9	496	9	US-09-864-761-2534	Sequence 2534, Ap
34	79.2	2.9	37265	13	US-10-087-192-49	Sequence 49, Appli
35	79.2	2.9	39443	16	US-10-085-117-313	Sequence 313, App
36	79	2.9	276	9	US-09-864-761-20595	Sequence 20595, A
37	79	2.9	462	9	US-09-864-761-3829	Sequence 3829, Ap
38	79	2.9	1728	16	US-10-189-507-2	Sequence 2, Appli
39	79	2.9	1728	16	US-10-189-507-2	Sequence 2, Appli
40	79	2.9	2308	9	US-09-927-267-2	Sequence 2, Appli
41	79	2.9	2366	13	US-10-302-172-351	Sequence 351, App
42	79	2.9	2551	10	US-09-842-758-29	Sequence 29, Appli
43	79	2.9	2551	13	US-10-174-333-29	Sequence 14, Appli
44	78.8	2.9	929	13	US-10-294-934-14	Sequence 15, Appli
45	78.6	2.9	143899	10	US-09-972-546-15	

ALIGNMENTS

RESULT 1

US-10-189-507-3
; Sequence 3, Application US/10189507
; Publication No. US20030228633A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PRONIN, ALEX
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: SERVANT, GUY
; APPLICANT: CALLAMARAS, NICHOLAS
; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
; TITLE OF INVENTION: SMELL MODULATORS
; FILE REFERENCE: 078003-0291567
; CURRENT APPLICATION NUMBER: US/10/189,507
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303,140
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337,154
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-189-507-3
Query Match 21.4%; Score 577.4; DB 16; Length 2607;
Best Local Similarity 64.3%; Pred. No. 9.6e-119;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
QY 679 TTCGAACAGCATGATTTCATACAGATCGACTTATCTCCCTGCTCTTCTGCTCA 738

Db 782 TCCCCAGAGCATGACCCCGCTGACCAACCTGATGTATGCTATGCTGTCTTCGCTGG 841
QY 739 CTCTTCCCTATAACTGGAACCTGCTGTTTATACCACTGGCGCTGCTCTTCCCATATCAA 798
Db 842 TGATGSCCTGGAATGGAACTGTTGGCTGNTTCCCGTGGCTGGGCTTCCCTTACCAGA 901
QY 799 CGCAGACAACATACACTCTGGCTTATGCGGACATCATATGTGATATCATCTACCTTT 858
Db 902 CCGGAGACAATCCACCACTGGCTGCTGATGATTAACCTATGCGACCTCATCTACTTCC 961
QY 859 ATGATATGCTATTTATTCAGCCAGACCTCCAGTTTGTAAAGGAGAGACATATAGTGG 918
Db 962 TGGACATACCGTGTTCAGACACCGCTGCACTTGTTCAGAGCGGGGAGACATCATACGG 1021
QY 919 ATTCAATGAGCTAAGGAAACACTACAGACTTCTACAAAATTTTCAGTTGGATGTCGCAT 978
Db 1022 ACAAAGGACATGCGAATAACTACCTGAAGTCTCGCGCTTCAAGATGACCTGTCTCA 1081
QY 979 CAATAATACCATTTGATATTTGCTTACCTCTCTTTGGGTTTAAATCCAAATGTTTAAAGCAA 1038
Db 1082 GCTCTCGCTGCTGATTTCTCTATTTGAAAGTGGTGTGAACCCCTCTCCGCTGCTG 1141
QY 1039 ATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCACTAGAGTCTATATAGG 1098
Db 1142 CCGCTGTTTAAAGTACATGCTCTTTCAGTTTAAAGGCGCTGGAATCCATCTCA 1201
QY 1099 ACAAGCATATATACAGAGTTATCGAAACAATGATCTTCTGTTTATTCGACCA 1158
Db 1202 GCAAGCTTACGTGACAGGCTATCAGACACAGCTTACCTTCTTACAGCCTGCATT 1261
QY 1159 TTAAGCTCTGTTTATTTACTGGCTTCAAACTATGAAGGAAATGGCACTACTAGATGG 1218
Db 1262 TGAATCTCTTCTTATTTACTGGGATCGGCTTATCAGGCTCGGCTCCACTCAGTGG 1321
QY 1219 TGTATGAGGGAAGAAACAGATATCTGATGATTTATTTGGGCAAGTTTCAACTTTAA 1278
Db 1322 TTTACGATGGCTGGAAACAGTTATTTCTGCTGTACTTCTTGTGTGAAGCCCTCA 1381
QY 1279 TTACATTTGGCTTCCAGAACCAAACTTTATTTGAATTTGTTTCACTCTGA 1338
Db 1382 TCACATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTGCTTCCAGCTGCTGA 1441
QY 1339 ATTTTCTGAGTTTCTGTTCTCCAGTTTAAATTTGCTGATGAGAGATGTGATTG 1398
Db 1442 ATTTTTCACGGCTGCTTGTCTTCTGATGATCGGACAGATGAGAGATGTGTTAG 1501
QY 1399 GAGCAGCTACAGCAATCAGAACTCTTCGGCTGCTGATGATGACACCACTTGCCTTACA 1458
Db 1502 GGGCGGCAACCGGGGACAGACTTACTACCGGAGCTGATGAGCAGCAGCAGCTGAAATGA 1561
QY 1459 TGAACAAATTTACTCCATTTCTTAACTTGTGAAAGCGAGTTTCGACTTGTGATGATATA 1518
Db 1562 TGAATTTCTACAGATCCCAAGTCCGTGAGAACCCGCTCAAGACTGTGACGATGA 1621
QY 1519 CATGGGACTCTCAAGAAATGATAGATGCTGATTTGCTTAAAGCCCTACCAACTACGG 1578
Db 1622 CTTGGCACTCGCAAGGATGCTGGATGATGATGATGATGATGATGATGATGATGATGAT 1681
QY 1579 TCAGTTTGGCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
Db 1682 TGGGCTGGACCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1741
QY 1639 AGGGTGTGATACAGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1698
Db 1742 AGGGCTGTGACCGGAGATGATTTTGAATGCTGAAGAGGCTTCTGTTGCTTACC 1801
QY 1699 TGCTGTGATTTGCTGCAAAAGGAGAAATTCGCAAGAAATGATATATCATCAAGC 1758
Db 1802 TGCCCAACGACTATGTGCAAGAGGGGAGATCGGCTGAGATGTATCATCCAGG 1861
QY 1759 ATGGAAGTCCAAAGTTCTTGGAGCCCTGATGGTAAAGTTCTGTTTACTCTGAAAG 1818

Db 1862 CAGGCAAGTGCAGGTCTTTGGCGGCTGATGGAAATCTGTGCTGGTGACGCTGAAAG 1921
QY 1819 CTGGTCCGTGTTTGGAGAAATCAGCTTCTAGCAGAGAGAGAGAAACCGTCGAACATG 1878
Db 1922 CTGATCTGTGTTTGGAGAAATTAAGTTGCTGCTGTTGGGGCGGGAACCGGCGACGG 1981
QY 1879 CCAATGTGTGGCCCAAGGTTTCCAAATCTTTAACTCTAGACAAAAGAGCCCTCCAG 1938
Db 1982 CCAAGTGTGGCGCAGGGTTTACCACCTCTTCTATCTGATTAAGAGGACCTGAATG 2041
QY 1939 AAATTTCTAGTGAATTTACAGATTTTGAAGGATCTCTATGAAGAAAGCCAGAGTCTTT 1998
Db 2042 AGATTTTGTGCTATTTCTGAGTCTCAGAAGTTACTCCGGAAGAAAGCCAGGCGATGC 2101
QY 1999 TAAAGCAGAGGCTAAGACCGCAGAG 2025
Db 2102 TGGAAGCAACATAAGCCCAAGAGG 2128

RESULT 2
US-10-159-563-147
; Sequence 147, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56USII
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 4382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-147

Query Match 21.4%; Score 577.4; DB 16; Length 4382;
Best Local Similarity 64.3%; Pred. No. 1.3e-118;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
QY 679 TTCCAAACAGCATAGATTTCATACAGATCGACTCTATCTCTGTGGCTCTTGTCTGTCA 738
Db 1983 TTCCCCAGAGCATTGACCCGCTGACCAACCTGATGATGCTATGCTGTCTTCTGG 2042
QY 739 CTCTTGCCTATACTGGAACCTGCTGTTTATACCACTGGGCTCGTCTTCCATATCAA 798
Db 2043 TGATGGCTCGAAATTTGGAACCTGTTGGCTGATTCGCTGGGCTTCCCTTACCAGA 2102
QY 799 CCGAGACAAACATACACTACTGCTTATTTGGGACATCATATGATATCATCTACCTTT 858
Db 2103 CCGGAGCAACATCCACCACTGGCTGCTGATGATTAACCTATGCGACTCATCTACTTC 2162
QY 859 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTGAAGAGGAGAGACATAATAGTG 918
Db 2163 TGGACATCACCGTCTTCAGACACGCTGCACTTGTTCAGAGCGGGGACATCATTCAGG 2222
QY 919 ATTCAATGAGCTAAGAAACACTACAGGACTTCTCAAAAATTTCACTTGGATGCTCCAT 978
Db 2223 ACAAAGGACATCGGAAATTAATCTAGTCTCGCCCTCAAGATGAGCTGCTCA 2282
QY 979 CAATAATACCATTTGATTTGCTTACCTCTTCTTGGGTTTAAATCCAAATTTTAGAGCAA 1038
Db 2283 GCCTCTCGCTTGGATTTCTCTATTTGAAAGTGGTGTGAACCCCTCTCCGCTGC 2342
QY 1039 ATAGGATGTTAAAGTACACTTCTATTTTCAATTTAATCATCACCTAGACTCTATATAG 1098

;; PRIOR FILLING DATE: 2002-10-21
;; PRIOR APPLICATION NUMBER: US 60/423,809
;; PRIOR FILLING DATE: 2002-11-05
;; PRIOR FILLING DATE: 2002-11-05
;; PRIOR FILLING DATE: 2002-11-26
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 27
;; LENGTH: 2085
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(2085)
US-10-345-680-27

Query Match 4.9%; Score 132.8; DB 15; Length 2085;
Best Local Similarity 49.2%; Pred. No. 3.7e-19; Indels 31; Gaps 4;
Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;

QY 918 GATTCAAAATGAGCTAAGGAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCGA 977
DB 703 GATACCAACAGCTGTGGCAGCATTAACAGCAGCAGCAGTTCAGGTGGATGTTG 762
QY 978 TCAATAATACCATTTGATATTTGCTACCTCTCTTTGGGTTTA---ATCCAATGTTTGA 1034
DB 763 TCCTGTGTCCTCCCGACCTGGCTTACTTAAAGGTGGGCACAACTACCCAGAAGTGAGG 822
QY 1035 GCAAAATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCACCTAGAGTCTATA 1094
DB 823 TTCAACCGCTACTGAAGTTTCCGGCTCTTTGAAATCTTTGACCGCAGACAGACAAG 882
QY 1095 ATGGACAAGCATATATCTACAGATTATTCGAACACTGGATCTGTTGTTTATCTG 1154
DB 883 ACCAACTACCCCAATATGTTCCAGATTGGGAATGCTGTTGTACATTTCTCATCATC 942
QY 1155 CACATTAATCCCTGTTTATTACTGGCTTCAAACTATGAAGAAATGGCACTACTAGA 1214
DB 943 CACTGGAATGCTGCTACTTCTGCAATTTCCAAATTTCAAGTTCAATTTGGGACAGACTCC 1002
QY 1215 TGGGTGT-----ATGATGGGAAGGAACAGATATCTGAGA 1250
DB 1003 TGGGTCTACCAACACATCTCAATCCAGAGATGGGCGCTCTCCAGGAAGTACATTTAC 1062
QY 1251 TGTTATTAATGGGAGTGGCACTTTAATACCATTTGGTGGCTTCCAGAACCAAACT 1310
DB 1063 AGTCTCTACTGGTCCACCTTGACCTTACCACCAATGGTGAGACCCACCCCGGTGAA 1122
QY 1311 TTATTTGAATTTGTTTCAACTCTTGAATTTTCTCGAGTTTGTGTTCTCCAGT 1370
DB 1123 GATCAGAGATATCTTTTGGTGGTCTAGACTTCTTGGTGGGTGTTCTGATTTTGGCAC 1182
QY 1371 TTAATTTGGTCCAGATGAGATGTAATTTGGAGCAGCTACAGCAATCAGAACTACTCCG 1430
DB 1183 ATTTGGGCAATGCGGCTCCATGATCTCGAATATGAATGCTCAGCGGAGAGTTCCAG 1242
QY 1431 GCCTGCTAGATGACACCATTTGCTACATGAACAACTTCTCAATTCCTAACTTGTCAA 1490
DB 1243 GCCAAGATTGATTCATCAGCAGTATCATGCTGTTCCGCAAGGTCCACCAAGGACTTGG 1302
QY 1491 AAGCGAGTTCCGACTTGGTATGAATATACATGGAATCTTCAAGAAATGCTAGATGATCT 1550
DB 1303 ACGCGGTTATCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1362
QY 1551 GATTTGCTTAAGACCTACCACTACGCTCCAGTTAGCCCTCGCAATGATGTAATTC 1610
DB 1363 GAGGTGCTCAAGAGCCTCCAGCAAGCTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1422
QY 1611 AGCATCATCAGCAAGTCCAGTCTGTTCAAGGGTGTGATACACAGATGATTTATGACATG 1670
DB 1423 CACACGCTGAGAGAGTTTCGATCTTCCAGGACTGTGAGGAGGCGGCTGCTGGTGGAG 1482
QY 1671 TTGCTAAGATTGAATCCGTTCTCTATTTTGGCTGGTGAATTTTGTCTGCAAAAGGGAGA 1730

DB 1483 GTGCTGAAGCTGCGACCCACTGTGTTTCAGCCCTGGGATTTATATCTCAAGAGGGAGAT 1542
QY 1731 ATTGCAAGGAATGTTATATCATCAAGCATGGAGAAGTCCAAAGTCTTTGAGGCGCTGAT 1790
DB 1543 ATTGGGAAGGATGTACATCATCAACGAGGCAAGCTGGCCGTGGTGGTGGTGGTGG 1602
QY 1791 GGTACTAAAGTTCTGGTTACTCTCTGAAAGCTGGGTGGTGGTGGTGGTGGTGGTGGT 1849
DB 1603 GTCACCCAGTTCTGGTGT---CCTCAGGATGGCAGCTACTTCGGGGAGATCAGCATTTCTG 1659
QY 1850 ACCAGCAGGAGGAGGAACCGTCTGAACTGC 1879
DB 1660 AACATCAAGGGAGCAAGTCCGGGAACCGC 1689

RESULT 9
US-10-345-680-25
; Sequence 25, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46566, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012P/IRM.OWNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILLING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILLING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILLING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILLING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILLING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILLING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILLING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILLING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILLING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3486
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(2124)
US-10-345-680-25

Query Match 4.9%; Score 132.8; DB 15; Length 3486;
Best Local Similarity 49.2%; Pred. No. 4.9e-19; Indels 31; Gaps 4;
Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;

QY 918 GATTCAAAATGAGCTAAGGAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCGA 977
DB 742 GATACCAACAGCTGTGGCAGCATTAACAGCAGCAGCAGTTCAGGTGGATGTTG 801
QY 978 TCAATAATACCATTTGATATTTGCTACCTCTCTTTGGGTTTA---ATCCAATGTTTGA 1034
DB 802 TCCTGTGTCCTCCCGACCTGGCTTACTTAAAGGTGGGCACAACTACCCAGAAGTGAGG 861
QY 1035 GCAAAATAGGATGTTAAAGTACACTTTCATTTTGAATTTTAAATCATCACCTAGAGTCTATA 1094

```

Db      862  TTCACCGGCTACTGAGTTTCCGGCTCTTTGAAATCTTTGACCGCAGAGACAAGG 921
QY      1095  ATGGCAAAAGCATATATCTACAGAGTAATTCGAACAACCTGGATATCTGCTTTATCTG 1154
Db      922  ACCAACTACCCCAATATGTTCAAGATTGGGAACCTGGTCTGTATCTCATCATCATC 981
QY      1155  CACATTAATGCGCTGCTTTATTTACTTGGGCTTCAAACTATGAGGAATTTGGCACTACTAGA 1214
Db      982  CACTGGAATGCGCTGCATCTACTTTGCGCATTTCCAAAGTTTCATGTTTGGGACAGACTCC 1041
QY      1215  TGGGTGT-----ATGATGGGAAGGAAGAACGAGTATCTGAGA 1250
Db      1042  TGGGTCTACCCAAACATCTCAATCCAGAGCATGGCGCTCTCCAGGAAGTACATTTAC 1101
QY      1251  TGTATTAATTTGGGAGTTCGAATTAATTAATCACTTGTGGCTTCCGAACCAAACT 1310
Db      1102  AGTCTCTACTGCTCCACCTTGACCTTACCACTTACCACTTGTGTGAGACCCACCCCGTGA 1161
QY      1311  TTATTTGAAATTTGTTTCAACTCTTGAATTTTCTGAGTGTCTTCTGAGTCTTCCAGT 1370
Db      1162  GATGAGGAGTACTCTTTGCTGTGCTAGACTTCTTGTGGTGTCTGATTTTGGCCACC 1221
QY      1371  TTAATTTGCTCAGATGAGAGATGTGATTTGGAGAGCTACAGCCAAATCAGAACTACTTCCG 1430
Db      1222  ATTGTGGCAATGTGGGCTCCATGATCTCGAATATGAATGCTCACGGGAGAGTTCAG 1281
QY      1431  GCTCCTCAGTATGACACCAATGCTTACATGATTAATTAATTAATTAATTAATTAATTA 1490
Db      1282  GCCAAGATGATTCATCAAGAGTACATGATCTCGAATGCTCGAAGGTCACCAAGGACTTGG 1341
QY      1491  AAGCGAGTTCGAGCTTGTATGAATATATACATGGGACTCTCAAGAAATGCTAGATGAGTCT 1550
Db      1342  ACGCGGTTATCCGGTGTGTTGACTACCTGTGGGCAACAGAGAGCGGTGATGAGAAG 1401
QY      1551  GATTTGCTTAAGACCTACCACTACGCTCAGTTCAGTTCAGCTTGGGCTGCTGGTGGAGCTG 1510
Db      1402  GAGGTGCTCAAGAGCTCCCAAGAGCTGAGTGAAGCTGAGATCGCCATCAACGTCACCTG 1461
QY      1611  AGCATCATCAGCAAGTGCATCTTGTCAAGGTTGTGATACACAGATGATTTATGACATG 1670
Db      1462  GACAGCTGAAGAGTTCGATCTTCCAGACTGTGAGGAGAGGCTGCTGGTGGAGCTG 1521
QY      1671  TTGCTAAGATTAATTCGTTCTCTATTTGCTGGTGTGATTTGCTGCAAAAAGGGAGAA 1730
Db      1522  GTGCTGAAGCTGCGACCACTGTGTTGAGCCCTGGGATTTATATCTGCAAGAGGAGAT 1581
QY      1731  ATTGGCAAGGAATGTATATCATCAAGCATGAGAGTCCAAAGTCTTGGAGGCCCTGAT 1790
Db      1582  ATTGGGAAGAGATGTACATCATCAAGAGGCAAGCTGGCCGTGGTGGCTGATGATGGG 1641
QY      1791  GGTACTAAAGTTCTGGTTACTCTGAAAGCTGGGTCGTTGTTGGAGAAATCAGCCCTTCT- 1849
Db      1642  GTCACCCAGTTTCGTGGT---CCTCAGCGATGGCAGTACTTCCGGGAGATCAGCATTCG 1698
QY      1850  AGCAGAGGAGGAGGAGAACGTCGCAACTGC 1879
Db      1699  AACATCAAGGGAGCAAGTTCGGGNAACCGC 1728

```

```

RESULT 10
US-10-087-217-1
; Sequence 1, Application US/10087217
; Publication No. US20030100059A1
; GENERAL INFORMATION:
; APPLICANT: Aptus Genomics, Inc.
; APPLICANT: YAO, Yong
; APPLICANT: CAO, Liang
; TITLE OF INVENTION: No. US20030100059A1 Cell-Based Assays for G-Protein-Coupled Re
; TITLE OF INVENTION: Activities
; FILE REFERENCE: 53735-5004-US
; CURRENT APPLICATION NUMBER: US/10/087,217
; CURRENT FILING DATE: 2002-03-04

```

```

; PRIOR APPLICATION NUMBER: 60/330,663
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1992)
; OTHER INFORMATION:
US-10-087-217-1

```

```

Query Match      4.9%; Score 131.6; DB 15; Length 1995;
Best Local Similarity 46.7%; Pred. No. 6.8e-19;
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;

QY      714  TATCTCTGCTGGCTCTGCTTGCCTCTTGCCTATTAAGTGAACCTGGTTTATACCA 773
Db      424  TATACCGTTGGTGTGCTTGCCTATTCGCAATGCTGTCTTTTCAACTGGTGGCTGTGGTG 483
QY      774  CTGCGCTCTGCTTCCCATATCAAAACCGCAGACAACATACACTACTGCTTATTCGGAC 833
Db      484  GCCAGAGCCTGCTTCAGTGATCTACAGAGAAACTATTTGTGGTATGCTGTGGTGGAC 543
QY      834  ATCATATGTATATCATCTTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTT 893
Db      544  TACTTCTCAGACACTGTCTATATCGAGACCTCATCATTCGGCTCGCACAGGC---TTC 600
QY      894  GTAAGAGGAGGAGACATATAGTGAATCAAAATGAGTAAAGGAAACACTACAGGACTTCT 953
Db      601  CTAGAACACGGGCTCTTGTCAAGATCCCAAGAAATTCGAGAGCAACTATATTCACACT 660
QY      954  ACAAATTTCACTGGATGCTGCATCAATAATACATTTGATATTTGCTACTGCTTCTTTT 1013
Db      661  TTCTGAGTTCAAAATGGATGTGGCTTCTATCATTCCTCCACTGACCTTATCTATTTGCTGTG 720
QY      1014  GGGTT---TAATCCAATGTTTAGACAAATAGGATGTTAAAGTACACATTCATTTTGA 1070
Db      721  GGTATCCACAGCCCTGAGGTAGCTTCAACCGTCTATTACACTTTGCCCGGTATGTTGAG 780
QY      1071  TTTAATCATCACTAGATCTATATTAAGCAAAAGCATATATCTACAGAGTTATTGCAACA 1130
Db      781  TTCTTTGACCGCACTGAGACAGCACCGACAGTACCCCAACATCTCCGAATCAGCAATCTG 840
QY      1131  ACTGATGACTTCTGCTTTTATTTCTGCACATTAATGCTGTGTTTATTTACTGGCTTCAAC 1190
Db      841  GTCCCTTTACATCTTGGTCATCATCCACTGGAATGCTGTATTTATTTATTTCTTAAG 900
QY      1191  TATGAAGGAATGG-----CACTACTAGATGGGTGTATGAT 1226
Db      901  TCCATTGGCTTGGAGTTGACACCTGGGTTTACCCCAACATTTACTGACCTGATATGTC 960
QY      1227  GGGGAAGGAACAGATATCTGAGATGTTTATTTGGGCAAGTTCGAACTTTAATTACCAAT 1286
Db      961  TACCTGGCTAGAGATACATTTACTGTCTTTACTGGTCCACACTGACCCCTCACCACT 1020
QY      1287  GGTGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTCAACTCTTGAATTTTTTT 1346
Db      1021  GGAGAGACACACCCCTGTAAAGGATGAGGAGTACCTATTTGTCACTTTGACTTCTTG 1080
QY      1347  TCTGGAGTTTGTGTTCTCCAGTTTAAATGCTCAGATGAGAGATGTTGATGGAGAGCT 1406
Db      1081  ATTGGTGTCTCATCTTTGCCACTATTGTGGAAATGTTGGGCTCCATGATCTCCAAACATG 1140
QY      1407  ACAGCCAATCAGAACTACTTCCGCGCTGCAATGATGACACCAATTTGCTCATCAACAAT 1466
Db      1141  AATGCCACACGAGAGAGTTCCAGGCCAAGATTGATGCTGTCAAACTACATGAGCTTC 1200
QY      1467  TACTCCATTCCTAACTTTGTGCAAAAGCGAGTTTCGGACTTGGTATGAATATACATGGGAC 1526
Db      1201  CGAAAGGTGAGAAAGAGATGGAAGCAAGGTATCAATGATGGTTTGAATCTACTTCTGTGAGCC 1260

```


QY 1527 TCTCAAGATGCTAGATGAGTCTGATTGCTTAAAGACCTACCAACTACGGTCCAGTTA 1586
Db 1261 AATAAGAGACAGTAGAAGAACGAGAGAGTCTCCAGAACCTGCCAGCAAGCTCAGGGCT 1320
QY 1587 GCCTCGCCATTGATGTGAACCTTACGATCATCAGCAAAAGTGCAGTTGTCAGGGTTGT 1646
Db 1321 GAGATAGCCATTAAATGTTCACTTGTCCACTCTGAGAGAAAGTGGCATAITTCAGGATTGT 1380
QY 1647 GATACACAGATGATTATGACATGTTGCTTAAGATTGAATCCCTTCTCTATTGTCCTGTT 1706
Db 1381 GAAGCTGGCCTACTGTGGAACTGGTACTGAAGCTTCGCTCCTCAGGTCTTTAGTCTCTGA 1440
QY 1707 GACTTTCTGTGCAAAAAGGAGAGAAATGGCAAGAAATGTATATCATCAAGCATGAGAGAA 1766
Db 1441 GATTATATTTGCCGTAAAGGGGACATTTGGCAAGAAATGTATCATCATCAAGGAGGCAAG 1500
QY 1767 GTCCAAAGTTCTTGAGGCCCTGATGTGATCACTAAAGTTCTGTGTTT---TACTCTGAAGCTGG 1822
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCGCTTGTCTCAGCTGGGAGCTGC 1560
QY 1823 GTGGTCTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAACCCGTCCAACTGGCC 1880
Db 1561 TTTGGTAGATTAGTATCTTACATTTAAGGTAGCAAAATGGCAATCGACGTACTGCT 1620
QY 1881 AATGTGTGGCCACCGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCCCTCCAGAA 1940
Db 1621 AATATCGTAGCTGGGCTACTCAGATCTCTTCTGCTTGTCCAGGACGATCTTATGGAA 1680
QY 1941 ATTCTAGTATATCAGATTTGAAAGGATCTCATGAAGAAAGCAGAGTCTTTTA 2000
Db 1681 GCTGTAACTAGTATCTGTATGCCAAGAGTCTCTGGAGGACGGGTAGGAGATCCTG 1740
QY 2001 AAGCAGAGGCT 2012
Db 1741 ATGAAGGAGCT 1752

RESULT 11

US-10-087-217-5
; Sequence 5, Application US/10087217
; Publication No. US20030100059A1
; GENERAL INFORMATION:
; APPLICANT: Aptus Genomics, Inc.
; APPLICANT: YAO, Yong
; TITLE OF INVENTION: Cell-Based Assays for G-Protein-Coupled Receptors
; TITLE OF INVENTION: Activities
; FILE REFERENCE: 53735-5004-US
; CURRENT APPLICATION NUMBER: US/10/087,217
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1992)
; OTHER INFORMATION:
US-10-087-217-5

Query Match 4.9%; Score 131.6; DB 15; Length 1995;
Best Local Similarity 46.7%; Pred. No. 6.8e-19;
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;
QY 714 TATCTCCGTGGCTCTTCTGTCATCTTCCCTATTAAGTCTGCTGTTTATACCA 773
Db 424 TATTACCGTTGGTCTTGTCTATGCCAATGCTGTTCTTTACAACTGGTCTGTTGGTG 483

QY 774 CTGGCCCTGCTTTCCCATATCAAAACCGCAGCAACATACACTACTGGCTTATTGGCGAC 833
Db 484 GCCAGAGCCTGCTTCAAGTATCTACAGAGAACTATTTTGGTATGGCTGGTGGAC 543
QY 834 ATCATATGATATCATCTACTCTTATGATATGATATTTATCCAGCCAGACTCCAGTT 893
Db 544 TACTTCTCAGACACTGCTATATCGCAGACTCATCATTCGGCTGGCAGAGC---TTC 600
QY 894 GTAAGAGGAGGAGACATATATAGTGATTCAAATAGCTTAAGGAACTACAGGACTTCT 953
Db 601 CTAGAACAGGGGCTCTTGGTCAAAAGATCCCAAGAAATTCGAGACAACTATATTCACT 660
QY 954 ACAAAATTTCAAGTTGGATGTCGATCATATATACCATTTGATATTTGCTACTCTTCTTT 1013
Db 661 TTGCAAGTTCAAAATGGATGTCGCTTCTATCATTCCTCAGCTTATCTATTGCTGTG 720
QY 1014 GGGTT---TAATCCAAATGTTTAGAGCAATAGGATGTTAAAGTATACACTTCAATTTTGA 1070
Db 721 GGTATCCACAGCCCTGAGTAGCTTCAACGCTCTATTACACTTTGCCCGTATGTTGAG 780
QY 1071 TTTAATCATCATCTAGAGTCTATTAATGGAAGAAAGATATCTACAGATTTATCGAACA 1130
Db 781 TTTCTTTGACCGCACTGAGACACGCAACCACTACCCCAACATCTTCCGAATCAGCAATCTG 840
QY 1131 ACTGGATCTTCTGTTTATCTGCACATTAATGCTGCTGTTTATTACTGGGCTTCAAC 1190
Db 841 GTCTTTTACATCTTGGTCAATCATCCACTGGAATGCTGTTTATTATGTTATTCTTAAG 900
QY 1191 TATGAAGGAATGG-----CACTACTAGATGGTGTATGAT 1226
Db 901 TCCATTGGCTTTGGAGTTGACACCTGGGTTTACCCTCAACATTTACTGACCTGAATATGGC 960
QY 1227 GGGGAAGGAAACGAGTATCTGAGATGTTATTATGGCAGTTCGAACCTTAAATACCATT 1286
Db 961 TACCTGGCTAGAGATACATTTACTGCTTTACTGGTCCACACTGCCCTCACCACATT 1020
QY 1287 GGTGGCTTCCAGAAACCAAACTTTATTGAAATTTGTTTTTCACTCTGTAATTTTTTT 1346
Db 1021 GGAGAGACACACCCCTGTAAGGATGAGGATACCTATTGTCATCTTTGACTTCTTG 1080
QY 1347 TCTGGAGTTTTGTTGTTCTCCAGTTTAAATGCTCAGATGAGAGATGTTGATGGAGCAGT 1406
Db 1081 ATTGGTGTCTCATCTTTGCCACTATTGTTGGAAATGTTGGGCTCCATGATCTCCAACTG 1140
QY 1407 ACAGCCCAATCAGAACTACTTTCGCCCTGCATGGATGACACCATTTGCCCTACATGAACAT 1466
Db 1141 AATGCCACAGCAGCAGAGTTCCAGGCCAGATTTGATGCTGCAACACTACATGAGTTTC 1200
QY 1467 TACTCCATTCTTAAACTTGTGCAAAAGCGAGTTGCGACTTTGGTATGATATATACATGGGAC 1526
Db 1201 CGAAAGGTGAGCAAAAGACATGGAAGCCAAAGTTCATCAATGTTGTTGACTTCTTTGGACC 1260
QY 1527 TCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAAGCCCTACCACTACGGTCCAGTTA 1586
Db 1261 AATAAGAACAGTAGATGAACGAGAGTCTTCAAGAACCTGCCAGCAAGCTCAGGGCT 1320
QY 1587 GCCTCGCCATTGATGTGAACCTTACGATCATCAGCAAAAGTGCAGTTGTTCAAGGGTTGT 1646
Db 1321 GAGATAGCCATTAAATGTTCACTTGTCCACTCTGAGAGAAAGTGGCATAITTCAGGATTGG 1380
QY 1647 GATACACAGATGATTTATGACATGTTGCTAAGATTGAATCCGTTCTCTATTGCTGCTGT 1706
Db 1381 GAAGCTGGCCTACTGCTGGAACCTGGTACTGGAAGCTTCTGCTCAGGTCTTTAGTCTCTGA 1440
QY 1707 GACTTTTGTCTGCAAAAAGGAGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGAGAA 1766
Db 1441 GATTATATTTGCCGTAAAGGGGACATTTGCCAGGAAATGTATCATCATCAAGGAGGCAAG 1500
QY 1767 GTCCAAAGTTCTTGAGGCCCTGATGTGATCACTAAAGTTCTGCTGTT---TACTCTGAAGCTGG 1822
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCGCTTGTCTCAGCTGGAGCTGC 1560
QY 1823 GTGGTCTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAACCCGTCCAACTGGCC 1880

Db 1561 TTTGGTGAATAGTATCTCTTAACATTAAGGTAGCAAAATGGGCAATCGACGTACTGCT 1620
Qy 1881 AATGTGGTGGCCACGGGTTTCCCAATCTTTTAACTCTAGACAAAGACCCCTCCAAGAA 1940
Db 1621 AATATCCGTAGCTGGGCTACTCAGATCTCTTCTGTTCTCAAGGACGATCTTATGAA 1680
Qy 1941 ATTCTAGTGCATATCCAGATTTCTGAAGGATCTCATGAAGAACCCAGAGTCTTTTA 2000
Db 1681 GCTGTAACGTAGTATCTCTGATGCCAAGAGGTCCTGGAGGAACGGGGTAGGAGATCCTG 1740
Qy 2001 AAGCAGAGGCT 2012
Db 1741 ATGAAGATGGGT 1752

RESULT 12
US-10-295-573-2
; Sequence 2, Application US/10295573
; Publication No. US20030157571A1
; GENERAL INFORMATION:
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schack, Jerome
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS
; FILE REFERENCE: UTC-07536
; CURRENT APPLICATION NUMBER: US/10/295,573
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/332,494
; FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3027
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-295-573-2

Query Match 4.9%; Score 131.6; DB 15; Length 3027;
Best Local Similarity 46.7%; Pred. No. 8.5e-19;
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;

Qy 714 TATCTCTGTGGCTTGTCTGCTCACTCTTCCCTATAACTGGAACCTGCTGTTTATACCA 773
Db 763 TATTACCCTGTGGTGTGTCTCAATGCGCATGCTGTTCTTACAACTGGTGGCTGTTGGTG 822
Qy 774 CTGGCCCTGCTTCCCATATCAACCCGACACACATACACTACTGCTTATTTGGGAC 833
Db 823 GCCAGAGCTGCTTCAAGTATCTACAGAAACTATTTTGGTATGGCTGGTGGTGGAC 882
Qy 834 ATCATATGTATATCATCTACTCTTATGATATGCTATTTATCCAGCCACAGACTCCAGTTT 893
Db 883 TACTTCTCAGACACTGTCTATATCGACACCTCATCTTCGGCTGCGCACAGGC---TTC 939
Qy 894 GTAAGAGAGAGACATATATAGTGGATTCATAGAGCTTAAGAAACACTACAGACTTCT 953
Db 940 CTGAACAGGGGCTCTTGGTCAAGATCCCAAGAAATTTGGAGCAACTATATTCACACT 999
Qy 954 ACAAAATTCAGTTGGATGTGCGCATCAATATACATTTGATATTTGCTACCTCTCTTT 1013
Db 1000 TTGCAGTTCAATTTGGATGTGGCTTCTATCTATCCCACTGACCTTATCTATTTGGTG 1059
Qy 1014 GGGT---TAATCAATGTTTAGAGCAATAGGATGTTAAAGTACATCTTCAATTTTGA 1070
Db 1060 GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTGCCCGTATGTTGAG 1119
Qy 1071 TTTAATCATCATCTAGTGTCTATATGACAAAGCATATATCTACAGATTTATTCGAACA 1130
Db 1120 TTTCTTACCCGACCTGAGACAGCCACAGCTACCCCAACATCTCCGAATCAGCAATCTG 1179
Qy 1131 ACTGGATACATGCTGTTTATTTCTGCATTAATGCTGCTGTTTATCTACTGGGCTTCAAC 1190

Db 1180 GTCTTTTACATCTTGTGTCATCATCCACTGGAATGCTTGTATTATTATTATGTTATTTCTAAG 1239
Qy 1191 TATGAAGGAATTTGG-----CACTACTAGATGGGTGTATGAT 1226
Db 1240 TCCATTTGGCTTTGGAGTTGACACCTTGGGTTTACCCCAACATTACTGACCCCTGAATATGGC 1299
Qy 1227 GGGGAAGGAACGAGATCTGAGATGTTTATTATTGCGGAGTTCGAACTTTTAATTAACCAT 1286
Db 1300 TACTCGCTAGAGATACATTTACTGTCTTTTACTGTCTCCACACTGACCCCTCAACCAT 1359
Qy 1287 GGTGGCTTCCAGAACCAAACTTTTATTGAAATTTGTTTTTCAACTCTTGAATTTTTT 1346
Db 1360 GGAGAGACACCCCTCTGAAGATGAGGAGTACCTATTTTGTCTATCTTTGACTTTCTTG 1419
Qy 1347 TCTGAGTTTGTGTTCTCCAGTTTAAATTTGTCAGATGAGAGATGTTGATTTGAGCAGCT 1406
Db 1420 ATTGGTGTCTCATCTTTGCCACTATTGTTGGAAATGTTGGGCTCCATGATCTCCAACATG 1479
Qy 1407 ACAGCCAATCAGAACTACTTCCGCCCTGCATGGATGACACCATTTGCCCTACATGACAAAT 1466
Db 1480 AATGCCACAGCAGAGATTTCCAGGCCAAGATTTGATGTGTCAAAACACTTACATGCAATTC 1539
Qy 1467 TACTCCATTCTTAAACTTGTGCAAAAGCGAGTTCCGACTTGTATGAATATATACATGGGAC 1526
Db 1540 CGAAAGGTGAGCAAGACATGGAAGCCAAAGGTCATCAATGTTGTTGACTTACTTTGGACC 1599
Qy 1527 TCTCAAGAAATGCTAGATGATGCTGTTGCTTAAGACCTTACCACTACGGTCCAGTTA 1586
Db 1600 AATAAGAACAGATGATGAACGAGAAGTCTTCAAGAACCTGCCAGAAAGCTCAGGCT 1659
Qy 1587 GCCTCGCCATTTGATGTGAATTTTCCAGCATCATCAGCAAAAGTCGACTTGTCAAGGGTGT 1646
Db 1660 GAGATAGCCATTAAATGTTTCCACTCTGAGAAAGTGGCATATTTCCAGATTTGG 1719
Qy 1647 GATACAGATGATTTATGACATGTTGCTAAGATTTGAAATCGTTCTTCTATTTGCTGGT 1706
Db 1720 GAAGCTGGCTACTGTTGGAATGTTGTAAGCTTCGCTCTCAGGCTTTTAGTCTTGA 1779
Qy 1707 GACTTTGTCTCAAAAGGGAGAAATTTGCAAGGAAATGTTATCATCAAGCATGGAGAA 1766
Db 1780 GATTATATTTGCGTATAGGGGACATTTGGCAAGGAAATGTTACATCATCAAGAGGGCAAG 1839
Qy 1767 GTCCAAAGTTTGGAGGCCCTGATGTTACTAAAGTTCTGGT----TACTCTGAAGCTGG 1822
Db 1840 TTGGCAGTGTAGCTGATGATGGCTGACTCAGTATGCTTGTCTCAGCTGGAGCTGC 1899
Qy 1823 GTCCGTGTTTGGAGAAATCAGCTTCTAGCAGCAGGAGGA--GGAAACGCTGCACTGCC 1880
Db 1900 TTTGGTGAATTAGTATCTTTAAATTAAGGTAGCAAAATGGGCAATCGACGTACTGCT 1959
Qy 1881 AATGTGTGGCCACGGGTTTGGCCAACTTTTAACTCTAGACAAAGACCCCTCCAAGAA 1940
Db 1960 AATATCCGTAGCTGGGCTACTCAGATCTCTTCTGCTTGTCCAGGACGATCTTATGAA 2019
Qy 1941 ATTCTAGTGCATATCCAGATTTCTGAAGGATCTCATGAAGAAAGCCAGAGTCTTTTA 2000
Db 2020 GCTGTAACGTAGTATCTCTGATGCCAAGAGGTCCTGGAGGAACGGGGTAGGAGATCCTG 2079
Qy 2001 AAGCAGAGGCT 2012
Db 2080 ATGAAGATGGGT 2091

RESULT 13
US-10-295-573-4
; Sequence 4, Application US/10295573
; Publication No. US20030157571A1
; GENERAL INFORMATION:
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schack, Jerome
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS


```

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12975
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013751.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.65
; US-09-864-761-12975

Query Match
Best Local Similarity 4.8%; Score 129; DB 9; Length 526;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 AGACAACTCTCCAGAAAATTCCTCTGGAGATCTGACCAAAACCCCTGACCTCAAAA 331
Db 191 AGACAACTCTCCAGAAAATTCCTCTGGAGATCTGACCAAAACCCCTGACCTCAAAA 250

QY 332 TGCAGCAGAACCAACTGCAAGTGCAGAGCAGAGCAAGAAATGACCCCGGAAAGAGG 391
Db 251 TGCAGCAGAACCAACTGCAAGTGCAGAGCAGAGCAAGAAATGACCCCGGAAAGAGG 310

QY 392 TCCAAACAG 400
Db 311 TCCAAACAG 319

RESULT 15
US-10-087-217-3
; Sequence 3, Application US/10087217
; Publication No. US20030100059A1
; GENERAL INFORMATION:
; APPLICANT: Aptus Genomics, Inc.
; APPLICANT: YAO, Yong
; APPLICANT: CAO, Liang
; TITLE OF INVENTION: No. US20030100059A1 Cell-Based Assays for G-Protein-Coupled Re
; TITLE OF INVENTION: Activities
; FILE REFERENCE: 53735-5004-US
; CURRENT APPLICATION NUMBER: US/10/087,217
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 60/330,663
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1992)
; OTHER INFORMATION:
; US-10-087-217-3

```

```

Query Match
Best Local Similarity 4.8%; Score 128.4; DB 15; Length 1995;
Matches 620; Conservative 0; Mismatches 676; Indels 36; Gaps 5;

QY 714 TATCTCCTGTGGCTCTTGTCTGTGTCACTTGTGCTATAAAGTGAACCTGCTGGTTATACCA 773
Db 424 TATTACCGTTGGTTGTTGTGCAATGGCATGCGCTGTTCTTTACACCTGGTGGCTGTGGTG 483

QY 774 CTGGGCTCGTCTTCCCATATCAACCGGAGACCAATACACTACTGCGGCTTATTCGGGAC 833
Db 484 GCCAGAGCCTGCTTCACTGATCTACAGAGAACTATTTTGTGTATGGTGGTGGTGGAC 543

QY 834 ATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTT 893
Db 544 TACTTCTCAGACACTGCTATATCGCAGACCTCATCTTCGGCTGGGACAGGC---TTC 600

QY 894 GTAAGAGGAGGAGACATAATAGTGATTCAAATAGAGTAAAGAAACACTTACAGGACTTCT 953
Db 601 CTAGAACAGGGGCTCTTGGTCAAGATCCCAAGAAATTCGAGACACTATATTCACACT 660

QY 954 ACATAATTTTCAGTTGATGTCGATCAATTAATACCATTTGATATTTGCTACCTCTCTTT 1013
Db 661 TTGCAGTTCAATTTGATGTCGCTTCTATCATTCACCTGACCTTATCTATTTGCTGTG 720

QY 1014 GGGTT---TAATCCAATGTTTAGAGCAATAGGATGTTAAAGTACACTTCATTTTGA 1070
Db 721 GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTGCCCGTATGTTGAG 780

QY 1071 TTTAATCATCACTAGACTATATATGACAAAGCATATATCTACAGAGTTATTCGAACA 1130
Db 781 TTCTTTGACGCTGAGACAGCAGCAGCTACCCCAACATCTTCGAAATCAGCAATCTG 840

QY 1131 ACTGGATCTTCTGCTTTTATCTGCACATTAATGCTGTTTATTTACTGGCTTCAAC 1190
Db 841 GTCTTTTACATCTTGTCTCATCATCCTGGAATGCTTGTATTTATTTATTTCTTAAG 900

QY 1191 TATGAAGAAATGG-----CACTACTAGATGGGTGTATGAT 1226
Db 901 TCCATGCTCTTGGAGTTGACACCTGGGTTTACCCCAACATTTACTGACCTGAAATATGGC 960

QY 1227 GGGGAAGAAACAGGATCTCGAGATGTTTATTTATTTGGGAGTTCGAACTTTAATTTACCAT 1286
Db 961 TACCTGGCTAGAGATGATTTACTGCTTTTCTGTTCCACACTGACCTCACCACCAT 1020

QY 1287 GGTGCTTTCCAGAACCAAACTTTTGAATTTTGAATTTTTCAACTCTTGAATTTT 1346
Db 1021 GGAGAGACACCCACCCCTGTAAAGGATGAGGATACCTATTTGTCTATCTTTGACTTCTTG 1080

QY 1347 TCTGAGATTTTGTGTTCTCCAGTTTAAATTTGTCAGATGAGAGATGATGGAGCAGCT 1406
Db 1081 ATTGGTGTCTCATCTTTGCCACTATTTGGGAAATGTTGGGCTCCATGATCTCCAAATG 1140

QY 1407 ACAGCCAATCAGAACTACTTCCGCGCTGTCATGGATGACACCACTTGTCTACATGAACAAT 1466
Db 1141 AATGCCACAGCAGAGTTCAGGCCCAAGATTGCTGTCAACACTACATGCACTGTC 1200

QY 1467 TACTCCATTTCTAACTGTGCAAAACGAGTTGCGACTTGGTATGATATACATGGGAC 1526
Db 1201 CGAAAGGTGAGCAAGACATGGAAGCCCAAGTCAATCAATGGTTTGACTACTTGTGGACC 1260

QY 1527 TCTCAAGAATGCTAGATGATGTTGTTTGAAGACCTTCAACACTACGCTCCAGTTA 1586
Db 1261 AATAAGAGACAGTAGATGAACGAGAGTCTCTCAAGACTGCGCAGCAAGCTCAGGGCT 1320

QY 1587 GCCCTCGCATTTGATGAACTTCAGCATCATCAGCAAACTGCACTGTTTCAAGGTTGT 1646
Db 1321 GAGATAGCCATTAATGTTCACTTGTCCACTCTCAAGAAAGTGGGCATATTTCCAGGATGT 1380

QY 1647 GATACACAGATGATTTATGACATGTTGCTAAGATTTGAATTCCTCTCTATTTGCTGCT 1706
Db 1381 GAAGCTGGCCTACTGTTGGAACTGTTACTGAACCTTCGCTCAGGCTTTTAGTCTCTGA 1440

QY 1707 GACTTTGTCTGCAAAAAGGAGAAATTTGGCAAGAAATGTATATCATCAAGCATGGAGAA 1766

```

Db 1441 GATTATATTTGCCGTAAAGGGGACATTGGCAAGGAAATGTACATCATCAAGGAGGGCAAG 1500
QY 1767 GTCCAAAGTTCTTGGAGGCCCTGTAGTACTAAAGTTCTTGGT----TACTCTGAAAGCTGG 1822
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGTGCTCAGTATGCCCTTGCTCAGCTGGGAGCTGC 1560
QY 1823 GTGGTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAAACCGTCGAACTGCC 1880
Db 1561 TTTGGTGAGATTAGTATCTTAAACATTAAAGGTTAGCAAAATGGGCAATCGACGTACTGCT 1620
QY 1881 AATGTGTGGCCCGCGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCCCTCCAAGAA 1940
Db 1621 AATATCCGTAGCCTGGGCTACTCAGATCTCTTCTGCTTGTCCAGGACGATCTTATGGA 1680
QY 1941 ATTCTAGTGCATTATCCAGATTCTGAAGGATCTCATGAAGAAAGCCAGAGTGCCTTTTA 2000
Db 1681 GCTGTAACTGAGGCTCTGTATGCCAAGAAGGTCCTGGAGGAACGGGGTAGGAGATCCTG 1740
QY 2001 AAGCAGAGGCT 2012
Db 1741 ATGAAGGAAGT 1752

Search completed: June 22, 2004, 09:37:11
Job time : 1120.37 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 17:15:34 ; Search time 9321.39 Seconds
(without alignments)
11299.126 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 agtcttaaatcgtgcacaaa.....aagaaaagctgaagcaataa 2430

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2430	100.0	4369	9	AF272900	AF272900 Homo sapi
2	2049.4	84.3	2135	9	AF228520	AF228520 Homo sapi
3	1682.2	69.2	2826	4	AF490511	AF490511 Canis fam
4	1362.4	56.1	4710	10	MMU243572	AJ243572 Mus muscu
5	577.4	23.8	3025	9	HUMCNCCC	L15297 Homo sapien
6	577.4	23.8	3408	9	HUMCNCCC	L15296 Homo sapien
7	577.4	23.8	4033	9	HUSU5837	U58837 Human CGMP-
8	577.4	23.8	4382	9	AF042498	AF042498 Homo sapi
9	575.2	23.7	4763	10	BC045114	BC045114 Mus muscu
10	572.2	23.5	3083	4	AF074012	AF074012 Bos tauru
11	572.2	23.5	3090	4	AF074013	AF074013 Bos tauru
12	572.2	23.5	3253	4	BTNCN4CGN	X94707 B.taurus mR
13	572.2	23.5	3290	4	AF074014	AF074014 Bos tauru
14	572.2	23.5	4282	4	BTNCN4CGN	X89626 B.taurus mR
15	569.6	23.4	4238	10	RNCNG41	AJ000496 Rattus no
16	568	23.4	4236	10	RNCNG43	AJ000515 Rattus no
17	568	23.4	4238	10	RNCNG43	AJ000515 Rattus no
18	330	13.6	205816	9	AC013751	AC013751 Homo sapi
19	237.4	9.8	2511	3	CEU73476	U73476 Caenorhadi
20	223	9.2	3358	3	BT001439	BT001439 Drosophi
21	217.8	9.0	3099	10	BC046523	BC046523 Mus muscu
22	196.2	8.1	441	10	AF015728	AF015728 Rattus no
23	187.4	7.7	1709	3	AY060725	AY060725 Drosophi
24	181.2	7.5	2061	4	SS085404	U85404 Sus scrofa
25	181.2	7.5	2857	9	S42457	S42457 CNGG=rod ph
26	176.8	7.3	2697	4	CFACGMP	X99914 C.familiari
27	176.8	7.3	2500	9	HUMCNCGMP	U83905 Canis fami
28	176.4	7.3	2500	9	HUMCNCGMP	M84741 Human CGMP-
29	173.6	7.1	2682	4	BTNCN4CGN	X51604 B.taurus RN
30	169.8	7.0	1874	9	AF547222	AF547222 Homo sapi
31	169.8	7.0	181804	9	AC107068	AC107068 Homo sapi
32	166.4	6.8	2297	10	MMU19717	U19717 Mus musculu
33	164.8	6.8	2474	10	MUSCNCG	M84742 Mus musculu
34	162.4	6.7	6312	3	AF091302	AF091302 Limulus p
35	161.4	6.6	58409	10	AL772281	AL772281 Mouse DNA
36	155.6	6.4	2612	5	GGRODCNG	X89599 G.gallus mR
37	152	6.3	2052	10	RNU48803	U48803 Rattus norv
38	150.6	6.2	200535	10	AL671880	AL671880 Mouse DNA
39	150.6	6.2	222330	2	AC099698	AC099698 Mus muscu
40	150.2	6.2	181805	2	AC114445	AC114445 Rattus no
41	150.2	6.2	190000	2	AC007704	AC007704 Homo sapi
42	150.2	6.2	233700	2	AC117107	AC117107 Rattus no
43	150.2	6.2	274011	2	AC096142	AC096142 Rattus no
44	148.8	6.1	2148	10	RNU93851	U93851 Rattus norv
45	139.6	5.7	2049	5	ICTCNC	M83111 Ictalurus p

ALIGNMENTS

RESULT 1
AF272900
LOCUS
DEFINITION Homo sapiens cone photoreceptor cyclic nucleotide-gated channel
beta subunit (CNGB3) mRNA, complete cds.
ACCESSION AF272900
VERSION AF272900.1 GI:9247065
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4369)
Kohl,S., Baumann,B., Broghammer,M., Jagle,H., Sieving,P.,
Keilner,U., Spegal,K., Anastasi,N., Zrenner,E., Sharpe,L.T. and

Wisinger, B.
 Mutations in the CNGB3 gene encoding the beta-subunit of the cone
 photoreceptor cGMP-gated channel are responsible for achromatopsia
 (ACHM3) linked to chromosome 8q21
 Hum. Mol. Genet. 9 (14), 2107-2116 (2000)
 20414632
 PUBLISHED
 10958649
 2 (bases 1 to 4369)
 Wisinger, B. and Kohl, S.
 Direct Submission
 Submitted (30-MAY-2000) University Eye Hospital, Molecular Genetics
 Laboratory, Auf der Morgensterle 15, Tuebingen D-72076, Germany
 Location/Qualifiers
 1. .4369
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 1. .4369
 /gene="CNGB3"
 47. .2476
 /gene="CNGB3"
 /codon_start=1
 /product="cone photoreceptor cyclic nucleotide-gated
 channel beta subunit"
 /protein_id="AAF86274.1"
 /db_xref="GI:9247066"
 /translation="MFKSLTKVKNKPIGENNENBQSRNNEGSHPSNOSQOQTAAOE
 ENKGEKSLKTKNSPTVSEEPHTNIQDLKSNSSGDLTNPDPQNAEPTGVPEBK
 EMDPEKSPNQKPPAPVINEYADQLNLVKNRQRTALYKKKLAVGDSUSPEA
 SPQAKPFAVPKESDDKPEHTEYRLRLFKVKKMPLTEYLKRIKJNSIDSYDRLY
 LLMLLVLAENKWFIPRLVFPYQADNIHWLADIICDIILYDMLFTQPRLLQ
 FVRGDIITVDNEKRLKHYRTSTKQLOVASIIPEDICYLFPFNPFRANRLKTYTF
 FEHNHLESIMDKAYIRVITGTGLFPLHINACVYVWASNYEGIGTTRVWYDGEN
 EYLCYVWAVATLTITGLPEPQTLFPIVFPOLLNFFVGVFVSLICQMRDVIQAATA
 NONPRAQMDITIAMNNYSIPKLVQKERTVETWDSORMLDESPLKTLPTTVOL
 ALADVNESIISKVDLPKCDTQMIYDMLRLKSLVLPDGFVCKKGEIKEMYIKH
 GEVVLGSPDSTKVLTLKAGSVFGBISLLAAGGNRRTANVAHGFAANLLTLDKKTL
 QEILVHPDSRILKKARVLLKQAKTAEATPPKDLALLFPKPEKPKFKTLGLG
 TGRASRLKLLKEQAAKKEEGEENEDKQENEDKQENEDKQENEDKQENEDK
 DKGREPEKPLDRPECTASPIAVBEEPSHVARIVLPRGTSRQSLIISMASBGGBEV
 LTVIEKKAQK"

Query Match 100.08; Score 2430; DB 9; Length 4369;
 Best Local Similarity 100.08; Pred. No. 0;
 Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGTTTAAATCGCTGACAAAAGTCAACAAAGTGAAGCTATAGGAGAGAACAAATGAGAAT	60
DB	47	ATGTTTAAATCGCTGACAAAAGTCAACAAAGTGAAGCTATAGGAGAGAACAAATGAGAAT	106
QY	61	GAAACAAAGTTCTGTCGAATGAAGAGGCTCTCACCCAAAGTATATAGTCTCAGCAAAAC	120
DB	107	GAAACAAAGTTCTGTCGAATGAAGAGGCTCTCACCCAAAGTATATAGTCTCAGCAAAAC	166
QY	121	ACAGCAGGAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC	180
DB	167	ACAGCAGGAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC	226
QY	181	ACGTCCTGAAGGCCACACCAACATACAGACAAATCTCTCAAGAAAAATTCCTCTGGA	240
DB	227	ACGTCCTGAAGGCCACACCAACATACAGACAAATCTCTCAAGAAAAATTCCTCTGGA	286
QY	241	GATCTGACCAACACCTCGACCTCAAAATGCAGCAGAACCACTGGAACAGTCCAGAG	300
DB	287	GATCTGACCAACACCTCGACCTCAAAATGCAGCAGAACCACTGGAACAGTCCAGAG	346
QY	301	CAGAAGGAAATGGACCCCGGAAAGAGGTCCTCAACAGCCCAACAAACAAACCGCTGCA	360
DB	347	CAGAAGGAAATGGACCCCGGAAAGAGGTCCTCAACAGCCCAACAAACAAACCGCTGCA	406
QY	361	GCTCCTGTATATATAGTATGCGATGCCAGTCCAGCTACACAACTGTGTAAGAAATGCGT	420

ORIGIN

Db	407	GCTCCTGTTTATAAATGAGTATGCCGATGCCAGCTACACAACTGCTGTAAGAAATGCGT	466
QY	421	CAAAGAACACCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCTCCTCACCCGAGCC	480
DB	467	CAAAGAACACCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCTCCTCACCCGAGCC	526
QY	481	AGCCCAAAACTGCAAGCCCGCAGGCTGTACACCACTGTAAGAAAGCGATGATAGCCA	540
DB	527	AGCCCAAAACTGCAAGCCCGCAGGCTGTACACCACTGTAAGAAAGCGATGATAGCCA	586
QY	541	ACAGAACATTACTACAGGCTGTGTGGTTCAAAGTCAAAAGATGCTTTAAACAGAGTAC	600
DB	587	ACAGAACATTACTACAGGCTGTGTGGTTCAAAGTCAAAAGATGCTTTAAACAGAGTAC	646
QY	601	TTAAAGCGAATTAACCTTCCAAACAGCATAGATTATACACAGATGCACTCTATCTCTG	660
DB	647	TTAAAGCGAATTAACCTTCCAAACAGCATAGATTATACACAGATGCACTCTATCTCTG	706
QY	661	TGGCTCTTGGCTCACTCTTGCTATAACTGGAAGTCTGCTGTTTATACCACTGCGCTC	720
DB	707	TGGCTCTTGGCTCACTCTTGCTATAACTGGAAGTCTGCTGTTTATACCACTGCGCTC	766
QY	721	GTCTTCCCATATCAAAACCGCAGACCAACATACACTACTGCTTATTGCGGACATCATGT	780
DB	767	GTCTTCCCATATCAAAACCGCAGACCAACATACACTACTGCTTATTGCGGACATCATGT	826
QY	781	GATATCATCTACTCTTATGATATGCTTATTATCCAGCCAGACTCCAGTTTGTAGAGA	840
DB	827	GATATCATCTACTCTTATGATATGCTTATTATCCAGCCAGACTCCAGTTTGTAGAGA	886
QY	841	GGAGACATTAATAGTGAATCAAAAGCTAAGCAAGCACTACAGGACTTCTACAAAATTT	900
DB	887	GGAGACATTAATAGTGAATCAAAAGCTAAGCAAGCACTACAGGACTTCTACAAAATTT	946
QY	901	CAGTTGGATGTCGATCAATATACATTTGATTTTGTCTCTCTTCTTGGGTTTAAAT	960
DB	947	CAGTTGGATGTCGATCAATATACATTTGATTTTGTCTCTCTTCTTGGGTTTAAAT	1006
QY	961	CCAATGTTTGTAGAGCAATAGGATGTTAAGTACATTTCAATTTTGAATTTAATCATC	1020
DB	1007	CCAATGTTTGTAGAGCAATAGGATGTTAAGTACATTTCAATTTTGAATTTAATCATC	1066
QY	1021	CTAGAGTCTATAATGGAACCAAGCATATATCTACAGAGTATTTCGAACAACTGGATCTG	1080
DB	1067	CTAGAGTCTATAATGGAACCAAGCATATATCTACAGAGTATTTCGAACAACTGGATCTG	1126
QY	1081	CTGTTTATTTCTGCACATTAATGCCCTGTGTTTATTTACTGGCTTCAAACTATGAGGAAT	1140
DB	1127	CTGTTTATTTCTGCACATTAATGCCCTGTGTTTATTTACTGGCTTCAAACTATGAGGAAT	1186
QY	1141	GGCACCTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATGG	1200
DB	1187	GGCACCTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATGG	1246
QY	1201	CGAGTTCTGCACTTTAATTAACCACTGGTGGCTTCCAGAACCAACAACTTTATTGAAAT	1260
DB	1247	CGAGTTCTGCACTTTAATTAACCACTGGTGGCTTCCAGAACCAACAACTTTATTGAAAT	1306
QY	1261	GTTTTCTCAACTCTTGAATTTTTTTTCTGGAGTTTTTTTGTGTTCTCCAGTTTAAATGGT	1320
DB	1307	GTTTTCTCAACTCTTGAATTTTTTTTCTGGAGTTTTTTTGTGTTCTCCAGTTTAAATGGT	1366
QY	1321	ATGAGAGATGATGGAGAGCTACAGCAATGAGAACTACTTCCGCGCTCGATGAT	1380
DB	1367	ATGAGAGATGATGGAGAGCTACAGCAATGAGAACTACTTCCGCGCTCGATGAT	1426
QY	1381	GACACCATTCCTACATGAACAAATTAATCTCCATTCTCTAACTTGTGCAAAAGCGAGTT	1440
DB	1427	GACACCATTCCTACATGAACAAATTAATCTCCATTCTCTAACTTGTGCAAAAGCGAGTT	1486
QY	1441	ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGATCTGATTTGCTTAAG	1500
DB	1487	ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGATCTGATTTGCTTAAG	1546

QY 1501 ACCCTACCACTACGGTCCAGTTAGCCCTCCGATTTGATGTGAATTCAGCATCATCAGC 1560
 Db 1547 ACCCTACCACTACGGTCCAGTTAGCCCTCCGATTTGATGTGAATTCAGCATCATCAGC 1606
 QY 1561 AAGTCGACTTGTTCACAGGGTGTGATACACAGATGATTTATGACATGTTGCTAAAGATTG 1620
 Db 1607 AAGTCGACTTGTTCACAGGGTGTGATACACAGATGATTTATGACATGTTGCTAAAGATTG 1666
 QY 1621 AATCCGTTCTATTTGCTGCTGGTGTGATTTGCTGCAAAAGGAGAAATGCGAAGGAA 1680
 Db 1667 AATCCGTTCTATTTGCTGCTGGTGTGATTTGCTGCAAAAGGAGAAATGCGAAGGAA 1726
 QY 1681 ATGTATATCATCAAGCATGGAAGTCCAAAGTCTTGGAGCCCTGATGGTACTTAAAGTT 1740
 Db 1727 ATGTATATCATCAAGCATGGAAGTCCAAAGTCTTGGAGCCCTGATGGTACTTAAAGTT 1786
 QY 1741 CTGGTACTCTCAAGCTGGTGGTGTGGAAGATCAGCTTCTAGCAGCAGAGGA 1800
 Db 1787 CTGGTACTCTCAAGCTGGTGGTGTGGAAGATCAGCTTCTAGCAGCAGAGGA 1846
 QY 1801 GAAACCCGTCGAATCCCAATGTGTGCGCCACCGGTTTGCAATCTTTAACTCTAGAC 1860
 Db 1847 GAAACCCGTCGAATCCCAATGTGTGCGCCACCGGTTTGCAATCTTTAACTCTAGAC 1906
 QY 1861 AAAAGAGCCCTCCCAAGAAATTTAGTCAATTTATCCAGATTTGAAAGATCTCTCATGAG 1920
 Db 1907 AAAAGAGCCCTCCCAAGAAATTTAGTCAATTTATCCAGATTTGAAAGATCTCTCATGAG 1966
 QY 1921 AAAGCCAGAGTGTCTTTAAAGCAGAGGCTTAAGACCCGAGCAAGCAACCCCTCCAAAGAAA 1980
 Db 1967 AAAGCCAGAGTGTCTTTAAAGCAGAGGCTTAAGACCCGAGCAAGCAACCCCTCCAAAGAAA 2026
 QY 1981 GATCTGCGCTCCCTCCCAAGAGAGAGACCCCAACCTGTTTAAACTCTCTTA 2040
 Db 2027 GATCTGCGCTCCCTCCCAAGAGAGAGACCCCAACCTGTTTAAACTCTCTTA 2086
 QY 2041 GGAGCAGAGAAAGCAAGTCTTCAAGACTACTCAAAATGAAGCAGAGCAAGCAGCT 2100
 Db 2087 GGAGCAGAGAAAGCAAGTCTTCAAGACTACTCAAAATGAAGCAGAGCAAGCAGCT 2146
 QY 2101 CAGAAGAAAGAAATTTGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
 Db 2147 CAGAAGAAAGAAATTTGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2206
 QY 2161 AAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAATGAAGATAA 2220
 Db 2207 AAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAATGAAGATAA 2266
 QY 2221 GATAAG 2280
 Db 2267 GATAAG 2326
 QY 2281 ATTGAGTGGAG 2340
 Db 2327 ATTGAGTGGAG 2386
 QY 2341 CGTCAATCACTATTATCAGATGGCTCTTCTGCTGAGGCGGAGAGAGAGAGAGAGAGAGAGAG 2400
 Db 2387 CGTCAATCACTATTATCAGATGGCTCTTCTGCTGAGGCGGAGAGAGAGAGAGAGAGAGAGAG 2446
 QY 2401 ATTGAAGTCAAGAAAG 2430
 Db 2447 ATTGAAGTCAAGAAAG 2476

RESULT 2
 AF228520
 LOCUS
 DEFINITION Homo sapiens cone photoreceptor cGMP-gated cation channel
 beta-subunit (CNGB3) mRNA, complete cds.
 ACCESSION AF228520
 VERSION AF228520.1 GI:8843947

KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2135)
 Sardin, O.H., Yang, J.M., Li, Y., Zhu, D., Hurd, J.N., Mitchell, T.N.,
 Silva, E.D. and Maumenee, I.H.

TITLE Genetic basis of total colourblindness among the Pingelapese
 islanders

JOURNAL Nat. Genet. 25 (3), 289-293 (2000)
 MEDLINE 20347712
 PUBMED 10888875

REFERENCE 2 (bases 1 to 2135)
 Sardin, O.H., Yang, J.-M., Li, Y., Zhu, D., Silva, E.D. and
 Maumenee, I.H.

TITLE Direct Submission

JOURNAL Submitted (25-JAN-2000) Ophthalmology, Johns Hopkins School of
 Medicine, 600 North Wolfe Street, Baltimore, MD 21287, USA

FEATURES
 source

1. 2135
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8q21-q22"
 /tissue_type="retina"
 1. 2135
 /gene="CNGB3"
 244..2076
 /gene="CNGB3"
 /note="membrane channel; CNGA3; core channel domain"
 /codon_start=1
 /product="cone photoreceptor cGMP-gated cation channel
 beta-subunit"
 /protein_id="AAF80179.1"
 /db_xref="GI:8843948"

gene
 CDS

1. 2135
 /translation="MPLTEYLKRIKLPNSIDSVTDRLYLILWLVLTVLWNNCCFPL
 RLNPYOTADNIHVLADIICDIIVLYDMFLQPLQFVRGDIIVDSNELRKHVYT
 STKEQLDVASIIIPEDICILFFGNPMFRANRLKYTSFEPFNHLSINDKAYIVKI
 RTGYLPLIHINACVITYWASNYEGITGRWIDGEGNLYRKYVWAVRLLITIGLPL
 EPQLFVIFOLLNFFSGVFESLIQMRDVIAGATNQNFACMDITIAIMNYS
 IPKLQKRVFTWYETWDSQRLDESLLKLTPTVQLALADVNFISIISKVDLFKGC
 DTOMIYMLRLKSLVLYLPGDFVCKEIGKENYIKHGEVQVLGPDGTQKVLVTLKA
 GSVLLAAGGNRRNTANVAFANLTLDKKLTQELIIVHPDSEILMKKARVLLKQK
 AKTAETAPPRKDLALLPPKPEETPKLFTLLGGTGKASLARLLKLKREDAOKKENSE
 GGEEGKENEKDKENEDKENEKDKREPEKPLDRPECTASPIAVEE
 EPHSVRTVLPRGTSRQSLIISMAPSAGGEEVLTIEVKEKAKQ"

ORIGIN
 Query Match 84.3%; Score 2049.4; DB 9; Length 2135;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 2075; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 340 CCACAAACAAACCGCTCGAGCTCCTGTTATTAATGATGATCGCATGCCGATGCCGCTACAC 399
 Db 1 CCACAAACAAACCGCTCGAGCTCCTGTTATTAATGATGATCGCATGCCGCTACAC 60

QY 400 AACCTGGTGAAGAAGATGCGTCAAGAACAGCCCTCTTACAGAAAAAGTTGGTAGAGGA 459
 Db 61 AACCTGGTGAAGAAGATGCGTCAAGAACAGCCCTCTTACAGAAAAAGTTGGTAGAGGA 120

QY 460 GATCTCTCTTACCCGAGGAGCCCAACACTGCAAGCCCGCCGCTGTACCCAGTGA 519
 Db 121 GATCTCTCTTACCCGAGGAGCCCAACACTGCAAGCCCGCCGCTGTACCCAGTGA 180

QY 520 AAAGAAAGCGATGATAAGCCCAACAGAACATTACTACAGGCTGTGTGGTTTCAAGTCAAA 579
 Db 181 AAAGAAAGCGATGATAAGCCCAACAGAACATTACTACAGGCTGTGTGGTTTCAAGTCAAA 240

QY 580 AAGATGCTTTACAGAGTACTTAAGCCGAATTAACCTCCAAACAGCATAGATTATAC 639
 Db 241 AAGATGCTTTACAGAGTACTTAAGCCGAATTAACCTCCAAACAGCATAGATTATAC 300

QY	640	ACAGATCGACTCTATCTCTCTGTGGCTCTTGCTTGTCACCTCTTGCCCTATAACTCGAAGTGC	699
DB	301	ACAGATCGACTCTATCTCTGTGGCTCTTGCTTGTCACCTCTTGCCCTATAACTCGAAGTGC	360
QY	700	TGGTTTATACCACTCGCGCTCGTCTCCCATATCAAAACCGCAGACAAATACACTACTCTGG	759
DB	361	TGTTTTATACCACTCGCGCTCGTCTCCCATATCAAAACCGCAGACAAATACACTACTCTGG	420
QY	760	CTTATTTGGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTTATCGAGCC	819
DB	421	CTTATTTGGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTTATCGAGCC	480
QY	820	AGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGGATTCAAATAGACTAAGGAACAC	879
DB	481	AGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGGATTCAAATAGACTAAGGAACAC	540
QY	880	TACAGGACTTCTACAAAATTTTCAGTTGAGTCGCATCAATAATAACATTTGATATTTGC	939
DB	541	TACAGGACTTCTACAAAATTTTCAGTTGAGTCGCATCAATAATAACATTTGATATTTGC	600
QY	940	TACCTCTCTTTGGGTTTAAATCCAAATGTTTAGACAAATAGGATGTTAAAGTACACTTCA	999
DB	601	TACCTCTCTTTGGGTTTAAATCCAAATGTTTAGACAAATAGGATGTTAAAGTACACTTCA	660
QY	1000	TTTTTTGAATTTAATCATCATCTAGAGTCTATATATGAGCAAGCATATATCTACAGAGTT	1059
DB	661	TTTTTTGAATTTAATCATCATCTAGAGTCTATATATGAGCAAGCATATATCTACAGAGTT	720
QY	1060	ATTCGAAACAACTGGATACCTCTCTGTTTATCTCGACATTAATGCTGTGTTTATTACTGG	1119
DB	721	ATTCGAAACAACTGGATACCTCTCTGTTTATCTCGACATTAATGCTGTGTTTATTACTGG	780
QY	1120	GCTTCAAACATANGAAGGAATGGCACTACAGATGGGTGTATGATGGGAAGGAACGAG	1179
DB	781	GCTTCAAACATANGAAGGAATGGCACTACAGATGGGTGTATGATGGGAAGGAACGAG	840
QY	1180	TATCTGAGATGTTATTATTGGGCAAGTTTCGAACCTTTAATTACCATTGGTGCCCTTCAGAA	1239
DB	841	TATCTGAGATGTTATTATTGGGCAAGTTTCGAACCTTTAATTACCATTGGTGCCCTTCAGAA	900
QY	1240	CCACAAACTTTATTGTAAATGTTTTTTCAACTCTTGAAATTTTTTTCTGGAGTTTTTGTG	1299
DB	901	CCACAAACTTTATTGTAAATGTTTTTTCAACTCTTGAAATTTTTTTCTGGAGTTTTTGTG	960
QY	1300	TTCTCCAGTTTAAATTGGTCAGATGAGAGATGCTGATTCGGACAGCTACAGCCATCAGAAC	1359
DB	961	TTCTCCAGTTTAAATTGGTCAGATGAGAGATGCTGATTCGGACAGCTACAGCCATCAGAAC	1020
QY	1360	TACTTCGCGCCTGCATGGATGACACCAATTCGCTACATGAACAATTACTCCATTCCTAAA	1419
DB	1021	TACTTCGCGCCTGCATGGATGACACCAATTCGCTACATGAACAATTACTCCATTCCTAAA	1080
QY	1420	CTTGTCBAAAGCGAGTTCGGACTTGATATACATGGGACTCTCAAGAATGCTA	1479
DB	1081	CTTGTCBAAAGCGAGTTCGGACTTGATATACATGGGACTCTCAAGAATGCTA	1140
QY	1480	GATGAGTCTGAATTTGCTTAAGACCTTACCAACTACCGGTCCAGTTAGCCCTCGCCATTGAT	1539
DB	1141	GATGAGTCTGAATTTGCTTAAGACCTTACCAACTACCGGTCCAGTTAGCCCTCGCCATTGAT	1200
QY	1540	GTGAATCTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTTGTGATACACAGATGATT	1599
DB	1201	GTGAATCTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTTGTGATACACAGATGATT	1260
QY	1600	TATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTGCTCGGTGACTTGTCTCTGCAA	1659
DB	1261	TATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTGCTCGGTGACTTGTCTCTGCAA	1320
QY	1660	AAGGGAGAATTTGGCAAGGAATGTATATCATCAAGCATGGAGAAGTCCAGTTCTTGA	1719
DB	1321	AAGGGAGAATTTGGCAAGGAATGTATATCATCAAGCATGGAGAAGTCCAGTTCTTGA	1380

[illegible]

Hungerford Hill Rd., Ithaca, NY 14853, USA

FEATURES
source

1..2826
/organism="Canis familiaris"
/mol_type="mrna"
/db_xref="taxon:9615"
1..2826
/gene="GNB3"
25..2373
/gene="GNB3"
/codon_start=1
/product="cyclic nucleotide gated channel beta subunit"
/protein_id="AA89224.1"
/db_xref="GI:2203793"
translation="MFKSLTIKSNKVKPRENDENKQDPDPSPNQSQSTROGENKSEN
KSLQNTKPTVTEESHAKMODKI SEKNRLDITNPNHOHPTESEKGMSEQKEMBTGK
EGLSPKSKPLGVPIVNEVADQLNLVRMEQRTMLYKKLAEQDIDSSPEASPTAK
LVTFSTQSNKLEKEHYHILCFKQKPLTEYLKSPFLPGSDISYDRLYLWLL
LVIAYNMCHWLIPLRVFPYQPDNTHFWITDIICDIIYLCDMLLQPLQFIKGG
DLMVDSNELKRHYRSTKQFDVASVMPDPVYLFPGFNPFVRMRILIKYTSFFBNH
HLESMIDKAYIRVIRITGGLYTLHINACIYVWASDYEGISTKRWYNGBNKYLR
YVWAVTLITIGLPEPQSFBIIVFOLLNFFSGVFSGLIQMDQDLPVTAATANQNF
RISMHTISYMTYSTPKNVONRVRTWYTVLWDSORMLDESLLCTLPVTMOLATVD
VNLISLVELPKGDQTMVYMLLKLKSTVYLPDGVCKGEIKGMWYIIKQGEVQV
LGSDQGVLTILKAGAVTEISLLAGRGNRRTANVIAHGEPANLLTLDKTLQELV
HYPDSKLLMKKAVLLKKAPATETTPPKGLAFLFPKQETPKI FRALLGGTQKAG
LTLKLRKEQTIQKTSSEEGGKRREYDEREPSEKILDSSECRANCIITASEMP
QSIRRAALPRGTTTQSLIISMAPSABAGEVLITIEVKEKAKQ"

ORIGIN

Query Match 69.2%; Score 1692.2; DB 4; Length 2826;
Best Local Similarity 83.8%; Pred. No. 3.4e-313; Indels 75; Gaps 3;
Matches 1972; Conservative 0; Mismatches 312;
QY 78 GAATGAAGAGGCTCTCACCAAGTAATCAGTCTCAGCAACCAACAGCAGCAGGAGAGAAA 137
DB 84 GATTAACAAGATCCTGATCCAGCAATCAGCCTCAGCAATCTACAAGACAGGAGAGAAA 143
QY 138 CAAAGGTGAAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCAGTGAAGAGCCACA 197
DB 144 CAAAAGTGAAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCAGTGAAGAAATCA 203
QY 198 CACCAACATCAAGACAAATCTCCAAAGAAATCTCTCGAGATCTGACCAACCAACCC 257
DB 204 TGCCAAATCGAAGATAATCTCCGGAATAATCTACTCAGAGACCTGACGACAAATCC 263
QY 258 TGACCTCAAAATCGACGAGAACCACTGAAACAGTGCACAGCAGAGAGAGAAATGACCC 317
DB 264 CAACCATCAACATCCAAACAGAAATCAAAAGGGGCAATGTCCAGAGCAGAGAGAAATG 323
QY 318 CGGGAAGAGAGGTCCAAACAGCCCAACAAACACACCGCTGACGCTCTGTTATAATGA 377
DB 324 TGGGAAGAGAGGCTAGTCAGCCCAAAAGCAACCCCTTGGAGTCCCTGTTATAATGA 383
QY 378 GTATGCGGATGCCAGCTACACACCTGTGTAAGAAATCGCTCAAGAACACGCCCTCTA 437
DB 384 GTATGCTGATCTCAGCTACACACCTGTGTAAGAAATCGCTCAAGAACAAATGCTCTA 443
QY 438 CAAGAAAGAGTGTGAGAGGAGATCTCTCTCAACCCGAGAGCCAGCCCAAACTGCAAA 497
DB 444 TAAGAAAGAGTGGCAGAGAGAGATATCTCTCACTGAAGCTAGCCCCCAAACTGCAAA 503
QY 498 GCCCAGCGCTGTACACAGTAAAGAAAGAGGATGATAAGCCAA--CAGAACATTACTA 554
DB 504 GCCCAGCGCTGTACATCAACAGAGAGAGCAATGCTAAGCTAAAGAAAGACATTACTA 563
QY 555 CAGGCTGTGTGTTCAAAAGTCAAAAGATGCCCTTTAAACAGAGTACTTAAAGCAATTA 614
DB 564 TCACATATTGTGTTTAAATTCAGAGAGATGCCCTCTGACAGAGTACCTAAAGCAATTA 623
QY 615 ACTTCCAAACAGCATAGATTCATACAGATCGACTCTATCTCTGTGGCTCTGTGCTGT 674
DB 624 ACTTCCAGGAAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTCTGTGCTGT 683

QY 675 CACTTTGGCCTATTAACCTGGAACTGCTGGTTTATACCACTGGCCTCGTCTTCCCATATCA 734
DB 684 CACCATTTGCTATAAATCGGAACCTGCTGGCTTATACCACTACGCTCGTCTTCCATATCA 743
QY 735 AACCGCAGACAAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCT 794
DB 744 AACACCAGACAAACACACTACTGGTTTATTACAGACATCATATGTGATATCATCTACCT 803
QY 795 TTATGATATGCTATTTATCCAGCCCACTCCAGTTTGTAAAGAGGAGGAGACATATAGT 854
DB 804 TTGTGATATGCTATTAATCCAGCCCACTCCAGTTTATATAAAGAGGAGGAGACATATAGT 863
QY 855 GGATTCAAATGAGCTAAGAAACACATACAGACTTCTTACAAAATTTTCAGTTGGATGTCG 914
DB 864 GGATTCAAATGAGTAAAGAGACACTACAGAGCTCTTACAAAATTTTCAGTTGGATGTCG 923
QY 915 ATCAATATATCACTTGTATATTTCTACTACCTCTCTCTTTGGGTTTAAATCCAAATTTAGAGC 974
DB 924 GTCAATATGCAATTTGATGTTTTTACCTCTCTCTTTGGGTTTAAATCCAGTATTTAGAT 983
QY 975 AAATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAAATCAATCACTAGAGTCTATAAT 1034
DB 984 GAATAGGATATTTGAAGTACACTTCAATTTTGAATTTTAAATCAATCACTAGAGTCTATAAT 1043
QY 1035 GGACAAAGCATATATCTACAGAGTTATTGCAAACTGGATCTTGTGTTTATTCTGCA 1094
DB 1044 GGACAAAGCATATATCTACAGAGTCTTGGAACTCTGATCTTGTATATATCTCTGCA 1103
QY 1095 CATTAAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGAAATTTGGCACTACTAGATG 1154
DB 1104 CATTAAATGCTGTGTTTATTACTGGGCTTCTGACTATGAAGAAATTTGGAAGTACTATAATG 1163
QY 1155 GGTGTATGATGGGGAAGGAAAGAGTATCTGAGATGTTATTATTGGGAGTTCGAACCTTT 1214
DB 1164 GGTGTATTAACGGTGAAGGAAACAAAGTATCTAAGATGTTATTATTGGGCTGTTCGAACCTTT 1223
QY 1215 AATTACCAATTTGGTGGCTTCCAGAACCAAACTTTATTGAAATTTGTTTTCAACTCTT 1274
DB 1224 AATTACCAATTTGGGAGCTTCCAGAACCAAACTTTATTGAAATTTGTTTTCAACTCTT 1283
QY 1275 GAATTTTCTTGGAGTTTGTCTCCAGTTTAAATTTGCTGAGTGAAGAGAGATGATG 1334
DB 1284 GAATTTTCTTGGAGTTTGTCTCCAGTTTAAATTTGCTGAGTGAAGAGATGATG 1343
QY 1335 TGGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTTGCATGATGATGATGATGATG 1394
DB 1344 TGGGAGCAGCCAGCCCAATCAGAACAACTTCCGAATCAGCATGATGATGATGATGATG 1403
QY 1395 CATGAACAAATTTACTCCATTTCTTAACTTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATA 1454
DB 1404 CATGAACAAATTTACTCCATTTCTTAACTTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATA 1463
QY 1455 TACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAAGACCTTACCAACTAC 1514
DB 1464 TACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATCTGCTCTGCAACCTGCTGCTCAC 1523
QY 1515 GGTCCAGTTAGCCCTCGCCATTTGATGTAACCTTACAGATCATCAGCAAAAGTCCGATTGTT 1574
DB 1524 CATGCAATTTAGCCCTCACTGTGATGTGAACCTCAGCATCATCAGCAAAAGTCCGATTGTT 1583
QY 1575 CAAAGGTTGTGATACAGATGATTTATGACATGTTTGTGATGTTTGAATTCGTTCTCTA 1634
DB 1584 CAAAGGTTGTGATACAGATGATTTATGACATGTTTGTGATGTTTGAATTCGTTCTCTA 1643
QY 1635 TTTGCTGTGATGTTTGTCTGCAAAAGGAGGAGAAATTTGCAAGAGAAATGATATCATCAA 1694
DB 1644 TTTGCTGTGATGTTTGTCTGCAAAAGGAGGAGAAATTTGCAAGAGAAATGATATCATCAA 1703
QY 1695 GAATGAGAGTCCAAAGTCTTGGAGGCTCTGATGTTTAAAGTCTTGGTACTCTGAA 1754
DB 1704 GCAAGGAGAGTCCAAAGTCTTGGAGGTTCTGATGTTGCTGCTTGGTACTCTGAA 1763

555 CAGGCTGTTGTTGTTCAAGATCAAAAGATGCTTTTAAACAGAGTACTTAAAGCGAATTAA 614
Db
617 CA---CGTTTTTTTCAAAACCCAGAGAGTCCAGTAAAGAGACCTTCAGAGAAATGAT 673
Qy
615 ACTTCCAAACAGCATAGATATCATACACAGATCGACTCTATCTCTGTCCTCTCTCTCTGT 674
Db
674 ACTTCCCAAGACATAGATCTCTACACAGATCGGCTCTATCTCTTGTGCTCTCTCTCTGT 733
Qy
675 CACTCTTGCTTAACTGGAACCTGCTGTTTATACCACTGCGCTCTGCTCTCTCTCTCTCTCT 734
Db
734 CACCATTGCTTAACTGGAACCTGCTGTTTATACCACTGCGCTCTCTCTCTCTCTCTCTCT 793
Qy
735 AACCGCAGACACATACACTACTCTGCTTATTCGGACATCATATGATGATATCATCTACT 794
Db
794 AACACAGATACAGAACTACTGATATTAAGATCTGATGATATCATCTACT 853
Qy
795 TTAATGATATGCTATTTATCAGCCAGACTCTGATTTTAAAGAGGAGAGACATATAGT 854
Db
854 TTGTGATATCTATTGATCCAGCAAGACTCCCAATTTGTAAGAGGAGGAGAAATATTGT 913
Qy
855 GGATCCAAATGAGCTAAGGAACACTACAGGACTCTCAAAATTTTCAAGTGGATGCTGCG 914
Db
914 AGATTCAAATGAGCTAAGGAACACTACAGGACTCTCAAAATTTTCAAGTGGATGCTGCG 973
Qy
915 ATCAATTAATACCAATTTGATATTTGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 974
Db
974 ATCTCTACTGCCATTCGAAGTCTCTACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1033
Qy
975 AAATAGATGTTAAAGTACACTTCAATTTTGAATTTATCATCATCTAGAGTCTATAT 1034
Db
1034 AAATCGGATATTAAGTATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1093
Qy
1035 GGCAAGACATATATACAGAGTATTCGAACAACTGGATCTCTCTCTCTCTCTCTCTCTCT 1094
Db
1094 GGCACAAAGCATATGCTACAGAGTCTCCGAACAACTGGATCTCTCTCTCTCTCTCTCTCT 1153
Qy
1095 CATTATGCTGTTTATTTACTGGGCTTCAACTATTAAGGAATTTGGCACTACTAGATG 1154
Db
1154 CATTAAAGCTGTTTATTTACTGGGCTTCAACTATTAAGGAATTTGGCACTACTAGATG 1213
Qy
1155 GGTGTATGATGGGAGAGAAACAGATCTGAGATGTTATTTGGGCACTCTCGAACTTT 1214
Db
1214 GGTCTATTAATGGTGAAGCAACAGATCTGCGATCTTTATTTGGGCACTCTCGAACTTT 1273
Qy
1215 AATTACCAATTTGGGCTTCCAGAACCAAACTTTATTTGAATTTGTTTCAACTCTT 1274
Db
1274 AATTACTATCGGGGCTTCCAGAGCACAGACTTCATTTGAATTTGTTTCAACTCTT 1333
Qy
1275 GAATTTTTTCTGGAGTTTTTGTCTCCAGTTTAAATGTTTCAAGATGAGATGAT 1334
Db
1334 GAATTTTTTCTGGGCTTTTGTCTCCAGTTTAAATGTTTCAAGATGAGATGAT 1393
Qy
1335 TGGAGAGCTACAGCCAAATCAGAACTACTTCCGCGCTGATGATGATGACCACTTCCTTA 1394
Db
1394 TGGGCGAGCAACAGCCAAATCAGAACTACTTCCGCGCTGATGATGATGATGATGAT 1453
Qy
1395 CATGAACAATTTCTCAATTTCTTAACTTTGTCGAAACAGGATTCGGACTTGGTATGATA 1454
Db
1454 CATGAACAATTTCTCAATTTCTTAACTTTGTCGAAACAGGATTCGGACTTGGTATGATA 1513
Qy
1455 TACATGGGACTCTCAAGAAATGCTAGATGATGCTGATTTGCTTAAAGACCTTACCACTAC 1514
Db
1514 TACATGGGACTCTCAAGAAATGCTAGATGATGCTGATTTGCTTAAAGACCTTACCACTAC 1573
Qy
1515 GGTCCAGTTAGCCCTCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1574
Db
1574 AATGAGTTGCTATTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1633
Qy
1575 CAAGGTTGATACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1634
Db
1634 CAAGGTTGATACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1693
Qy
1635 TTTGCTGGTGAATTTGCTGCAAAAGAGGAGAAATTTGGCAAGGAATGATATATCATCA 1694

1694 TTTACCTGGTGAATTTGCTGCAAAAGAGGAGAAATTTGCAAAAGAAATGATATCATCA 1753
Qy
1695 GCATGGAGAGTCCAGTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGAT 1754
Db
1754 ACAGGAGAGTCCAGTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGAT 1813
Qy
1755 AGCTGGGCTGGTGTGTTGGAGAAATCAGCTTTAGCAGCAGGAGGAGAAACCGTCAAC 1814
Db
1814 AGCTGGGCTGATGTTTGGAGAAATCAGCTTTGCGCAAAAGAGGAGGAGAAATGCGCG 1873
Qy
1815 TGCCAAATGTTGGTGGCCCAAGGTTTCCAAATCTTTAACTCTAGACAAAAGACCTTCCA 1874
Db
1874 AGCTGATGTTTGGTGGCCCAAGGTTTCCAAATCTTTAACTCTAGACAAAAGACCTTCCA 1933
Qy
1875 AGAAATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1934
Db
1934 AGAAATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1993
Qy
1935 TTTAAAGCAGAGGCTTAAGCCGAGAGCAACCCCTCCAAAGAAAGATCTTGGCCTCT 1994
Db
1994 TTTAAAGCAGAGGCTTAAGCCGAGAGCAACCCCTCCAAAGAAAGATCTTGGCCTCT 2053
Qy
1995 CTTCCCAAG 2054
Db
2054 TTTCCCAAG 2113
Qy
2055 AGCAAGTCTTCAAGAGTACTTCAAAATGAAAGCAGAGCAACCCCTCCAAAGAAAGAT 2114
Db
2114 GGTGAGCTTGGAGAGTCTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2164
Qy
2115 TTTCAAGGAG 2174
Db
2165 -----ATTAAGTGAAGTTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2195
Qy
2175 TAAACAAAAG 2234
Db
2196 AAG 2246
Qy
2235 GCCAG 2294
Db
2247 -----AAAAAACCCACCTGGATGAGTTCAGAGGAGAGAGAGAGAGAGAGAGAGAG 2301
Qy
2295 AGAACCCACCTCAGTTAG 2354
Db
2302 AATGTTCCCAATCAATTAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2361
Qy
2355 TATCAGATGCTCTCTCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2414
Db
2362 CAGCAACATGG-TCTGCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2420
Qy
2415 AAGGCTAAGCAATTA 2430
Db
2421 AAGGCTAAGCAATTA 2436

RESULT 5

HUMNGCCB

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

HUMNGCCB 3025 bp DNA linear PRI 01-MAY-1995
Homo sapiens clone hRNC2a retinal rod cyclic nucleotide-gated
cation channel gene, complete cds.

L15297
L15297.1 GI:291914
cyclic nucleotide-gated cation channel; retinal protein.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3025)

Chen, T.Y., Peng, Y.W., Dhalluin, R.S., Ahmed, B., Reed, R.R. and

Yau, K.W.

A new subunit of the cyclic nucleotide-gated cation channel in

retinal rods

JOURNAL Nature 362 (6422), 764-767 (1993)
 MEDLINE 93226050
 PUBLISHED 7682292
 REFERENCE 2 (bases 1 to 3025)
 AUTHORS Ahamed, B.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAY-1993) Basheer Ahamed, Biomedical Engineering,
 Johns Hopkins School of Medicine, Baltimore, MD 21205, USA
 COMMENT Original source text: Homo sapiens DNA.
 FEATURES Location/Qualifiers
 source
 1..3025
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="hRNC2a"
 /tissue_type="retinal"
 589..2460
 CDS
 /codon_start=1
 /product="cyclic nucleotide-gated cation channel"
 /protein_id="AA05619.1"
 /db_xref="GI:790520"
 /translation="MLCKFKHPKKYQPPQSIDPLNLMYVLWLFVVMANWNCW
 LIPVRAPPTQPNIRHLLMDYLCLITFDITVQTRLQFVRGDIITDKKMRN
 NYLRRFKMLLSLLPDLFLYKGVNPLRLPRCLKYNWAFEFNRSLEILSKAY
 YRVIRTYALLSLHNSCLYMASAYQGLSTHWYDVGVSYIRCYEPAVKLLTI
 GGLDPKTLFEIVQLLNYFTGVPAFVSMIQMRDVVGAATAGTQTYRSCMDSTVKYM
 NFYKIPKSVQRNLTWYEVYTHWSQMLDESELMVOLPKMRLDLADVINYISKVL
 FQCGDROMI PMLKRLSVVLPNDYVCKGELGEMVYIIQAGOVOLGSPDGKSLV
 TLKAGSVGEISLLAVGGNRRTANVAHGFNLFLDKDLNEILLVHPESQKLRLK
 KARRMLSNKPKKEKSVLIIPPRAGTTPKLFNALAMTGMKGKAGKGLAHLRL
 KELAALBAAKHSELVQAKSODVKGEGSAAPDQHTPKBAATPPAPRTPPPG
 SPPSPPPASLGCEGEEGPAEPHESVIRICMSPGPEPGEILSVKMPERBEKAE"

ORIGIN

Query Match 23.8%; Score 577.4; DB 9; Length 3025;
 Best Local Similarity 64.3%; Pred. No. 6.1e-101;
 Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

Qy 617 TTCAAACAGATAGATTACACAGATCGACTCTATCTCTGTGGCTCTTGTGTC 676
 Db 635 TTCCCCAGAGCATTTGACCGCTGACCAACCTGATGATGCTATGCTTCTTCTG 694
 Qy 677 CTCCTGCTATACTGGAATGCTGTTTATACACTGCGCTCGCTTCCCATATCAA 736
 Db 695 TGAATGGCTGGAATTTGAATGCTGTTGCTGATTCCTGCTGCGCTTCCCTACCA 754
 Qy 737 CCGCAGACAAACATACATCTACTGCTTATGGGACATCATATGATATCATCTACT 796
 Db 755 CCGCGACAAACATCCACCTGCTGCTGATGATTAACCTATGCGACCTCATCTTCC 814
 Qy 797 ATGATATGCTATTATTCAGCCAGATCTCAGTTTGAAGAGGAGAGACATATAGTGG 856
 Db 815 TGGACATCACCGTGTTCAGACACGCTGCGATTTGTCAGAGGCGGGGACATCATACGG 874
 Qy 857 ATTCAAATGAGCTAAGGAAACATACAGGACTTCTACAAAATTTCAAGTTGAGTGC 916
 Db 875 ACAAAGGACATCGGAAATAACTACCTGAGTCTGCGCCCTCAAGATGGACCTGCTCA 934
 Qy 917 CAATAATACCATTTGATTTGCTACTCTCTTTTGGTTTAAATCCAAATTTTAGAGCAA 976
 Db 935 GCCTCTCGCTTGGATTTTCTATTTGAAGTGGTGTGAACCCCTCTCCGCTGCG 994
 Qy 977 ATAGATGTTAAAGTACACTTCTATTTTGAATTTAATCATCATACCTAGAGTCTATATGG 1036
 Db 995 CCGCTGTTTAAAGTACATGGCTTCTTCAAGTTTAAACAGCCGCTGGAATCATCTCA 1054
 Qy 1037 ACAAGCATATATACAGAGTTATTGCAACAACTGATACCTTGTCTTATCTGCACA 1096
 Db 1055 GCAAGCCTACGTGTACAGGCTCATCAGGACCAACAGCTACCTTCTCTACAGCTGCATT 1114
 Qy 1097 TTAATGCTGTTTATTAATGCTGCTTCAACTATGAGGAATTTGGCACTACTAGATGG 1156
 Db 1115 TGAATTCCTGCTTTTATTAATGCTGCTTCAAGGCTTATCAGGCTTCTGCTCACTGCT 1174

Qy 1157 TGTATGATCGGGAAGAAACAGATATCTGAGATGTTATTTATTTGGCAGTTCGAACCTTAA 1216
 Db 1175 TTTACGATGGCGTGGGAAACAGTATATTCGCTGTACTTCTTCTGTGAAGACCTCA 1234
 Qy 1217 TTACCAATTCGTCCTCCAGAACACAACTTTATTTGAATTTCTTTTCAACTCTTGA 1276
 Db 1235 TCACCAATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTCTTCCAGCTGCTGA 1294
 Qy 1277 ATTATTTTCTGAGATTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGATGTGATTG 1336
 Db 1295 ATTATTTTCAAGGCTGTTTCTTCTGTGATCATCGGACAGATGAGATGTGGTAG 1354
 Qy 1337 GAGCAGTACAGCAATCAGAACTACTTCCGGCTGATGATGATGATGATGATGATGATGATG 1396
 Db 1355 GGCGCGCCACCGCGGACAGACTTACCGCAGCTGATGATGATGATGATGATGATGATGATG 1414
 Qy 1397 TGAACAAATTTACTCCATTCCTAACTTTGCAAAAGCAGTTTCGGACTTTGGTATGAATATA 1456
 Db 1415 TGAATTTCTACAAGATCCCAAGTCCGTGCGAAGCCGCTCAAGACCTGTGTACAGTACA 1474
 Qy 1457 CATGGACTCTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGATG 1516
 Db 1475 CCTGGCACTCGAAGGCATGCTGGATGATGATGATGATGATGATGATGATGATGATGATG 1534
 Qy 1517 TCCAGTTAGCCCTCCCAATTTGATGAACTTTCAGCATCATCAGCAAAAGTTCGACTTGTTC 1576
 Db 1535 TCGGCTGCACTCCCAATTCAGCTGAACTACACATCTGTAGCAAGTTCGACTTGTTC 1594
 Qy 1577 AGGTTGTGATACACAGATGATTTATGACATGTTTGTCTAAGATTTGAAATTCGTTCTTAT 1636
 Db 1595 AGGCTGTGTCGCGGACAGATGATTTTGCATGCTGAGAGGCTTCGCTCTGTTCTTACC 1654
 Qy 1637 TCCTGTGTGACTTCTCTGCAAAAGGAGAAATTTGCAAGAAATGATATATCATCAAGC 1696
 Db 1655 TCCCAACAGACTATGTGCAAGAGAGGAGATTCGCGCTGAGATGATGATGATGATGATGATG 1714
 Qy 1697 ATGGAGAAATCCAACTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATG 1756
 Db 1715 CAGGCAAGTGCAGTCTTGGCGCCCTGATGATGATGATGATGATGATGATGATGATGATG 1774
 Qy 1757 CTGGTCTGCTTTGGAGAAATCAGCTTCTAGCAGAGGAGGAGAAACCGTGCAGACTG 1816
 Db 1775 CTGGATCTGTTTGGAGAAATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1834
 Qy 1817 CCAATGCTGGTGGCCACCGGTTTGCATCTTTAACTCTAGACAAAAGACCTCCCAAG 1876
 Db 1835 CCAAGCTGTTGGCGACCGGTTTACCACTTCTTCTCTGATGATGATGATGATGATGATG 1894
 Qy 1877 AAATTTCTAGTATTCAGATTCAGAAATGATGATGATGATGATGATGATGATGATGATGATG 1936
 Db 1895 AGATTTTGTGATTTATCTGATGCTCAGAGTTTACTCCGGAAGAAAGCCAGGCGCATGC 1954
 Qy 1937 TAAAGCAGAGGCTAAGACCGCAGAG 1963
 Db 1955 TGAGAGCAACATAAGCCCAAGSAGG 1981

RESULT 6

HUMNGCCA

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Yau, K.W.

HUMNGCCA 3408 bp DNA linear PRI 01-MAY-1995
 Homo sapiens clone hRNC2b retinal rod cyclic nucleotide-gated
 cation channel gene, complete cds.

L15296
 L15296.1 GI:291913

cyclic nucleotide-gated cation channel; retinal protein.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3408)

Chen, T.Y., Peng, J.W., Dhallan, R.S., Ahamed, B., Reed, R.R. and

Yau, K.W.

TITLE
 A new subunit of the cyclic nucleotide-gated cation channel in
 retinal rods
JOURNAL
 Nature 362 (6422), 764-767 (1993)
MEDLINE
 93226050
PUBMED
 7682292
REFERENCE
 2 (bases 1 to 3408)
AUTHORS
 Ahmed, B.
TITLE
 Direct Submission
JOURNAL
 Submitted (17-MAY-1993) Basheer Ahmed, Biomedical Engineering,
 Johns Hopkins School of Medicine, Baltimore, MD 21205, USA
COMMENT
 Original source text: Homo sapiens DNA.
FEATURES
 Location/Qualifiers
 1..3408
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="hRCNC2b"
 /tissue type="retinal"
 105..2834
 /codon_start=1
 /product="cyclic nucleotide-gated cation channel"
 /protein_id="AAA5620.1"
 /db_xref="GI:790511"
 /translation="MPREISRIEEDDEEEDEEEEEEVTEVLDDSCVVSQVG
 VGSDEARASQVPATKQHPVEQVEDTDADSPCLMAEENPPSTVLPSPSPAKSDFTKI
 EPEAEAEAEASQVATKQHPVEQVEDTDADSPCLMAEENPPSTVLPSPSPAKSDFTKI
 VPSASGTHRKLKLPSEDDERAEELKALSPAESPVAKSDPTTPKDTQDQRAASTASTN
 SALINDQLBLVLFKFERKEKKEKLIDPDVTSDESPKSPAKPAPEAPDTKPAEA
 EPEVEEHCDMLCKFKERKPKWKYQFPQSDPLTNLMYVLVFFVYVMAWNNCNLLIP
 RWAFPYQPNITHHLLMDLYCLDIYFLDITVFTQLQFVRGGDIITDKDMRNWLLYK
 SRFPKDWLLSLLEPLFKVGNVPLLRCLKYMFAFEFNSRLSEIISKAYIVYRI
 RTTAYLLSHLNSCLVYASAYQGLSTHWYDVGNSYRCYFEAVKTLITIGLPL
 DKPTLFEIYQLLNLYFTGFAPFARMIGOMEDVVGATAGCTYVRSQMDSTVKVMFYK
 IPKSVQRVKTWTEYVHWSQGLMDESELVQLPDKMLDLAIDVYNIYKVALFOGC
 DRMI FDMKRLRSVLPNDYVCKGEIGREMI IQAGQVQLVGGDQKSVLUTLKA
 GVSGFETSLAVGGNRRTNVAHGFNLFLDKDLNLEILVHYPESOKLRLKARR
 MLRSNNPKKEKSVLILPPRAGTQPLFNALAMTKMGKAGXGGLARLKLRLKLA
 ALBAAKHBEVLQVAKSQQVKGEGSAAPODQTHPKAATDPAPRTPEPPGSPSPS
 SPPPASLGSCEGEEGPAEPHEHSVRIKMSPGPEPGEQILLVQKMPERBEKAE"
ORIGIN
 Query Match 23.8%; Score 577.4; DB 9; Length 3408;
 Best Local Similarity 64.3%; Pred. No. 6.1e-101;
 Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
 QY 617 TTCCAAACAGCATAGATTATACACACAGATCGACTCTATCTCTGTGCTCTTGTCTGTCA 676
 Db 1009 TTCCCCAGAGCAITGACCCGCTGACCAACCTGATGTATGCTTATGCTGTCTTCTTCTGTG 1068
 QY 677 CTCTTGCTCTATACTGGAATGCTGGTATTATACCACTCGCGCTCGTCTTCCCATATCAAA 736
 Db 1069 TGATGGCTTGAATTGGAATGTGGCTGATTCCTCGTGCGCTGCCCTTCCCTTACCAGA 1128
 QY 737 CCGCAGACACATACACTACTGGCTTATTCGGGACATCATATGTGATATCATCTACCTTT 796
 Db 1129 CCCCGGACACATCCACCATCTGGCTGCTGTGATGATGATGATGATGATGATGATGATGAT 1188
 QY 797 ATGATATGCTATTTTATCCAGCCACAGCTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGG 856
 Db 1189 TGGACATACCGTGTTCCAGACACGCTGCACTGTTGTTCAGAGCGGGGACATCATTTACGG 1248
 QY 857 ATTCAAATGAGCTAAGGAAACACATACAGGACTTCTTCAAAAATTTTCAAGTTGATGTCGAT 916
 Db 1249 ACAAAGGACATCGAAATAAATACCTACCTGAACTCTCCCGCTTCAAGATGACCTGTCTCA 1308
 QY 917 CAATAATACCATTTGATATTTGCTTACCTCTTCTTTGGGTTTAATCCAAATGTTTAGACAA 976
 Db 1309 GCCTTCCTGCCCTTGGATTTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCTCCGCTGC 1368
 QY 977 ATAGATGTTTAAAGTACACTTCATTTTGTGAATTTAATCATCACTAGAGTCTTAATAGG 1036
 Db 1369 CCCGCTGTTTAAAGTACATGAGCTTCTTCGAGTTTAAACAGCGCTTGAATCCCATCTCA 1428

QY	1037	ACAAACCATATCTACAGATTATTCGAACACTCGATACCTGCTGTTTATCTTCGACA	109
Db	1429	GCAAGCCACGTGTACAGGTCATCAGAGCACAGCTACCTTCTCAGAGCTGCAAT	1488
QY	1097	TTAATCCCTGTGTATTTACTTGGGCTTCAAACATGAAGAAATGGCACTACTAGATGGG	1156
Db	1489	TGAATTCCTGTCTTTATTTACTGGGCATCGGCTATCAGGGCTTCGGCTCCACTCACTGGG	1548
QY	1157	TGTATCGTGGGAAGGAACAGATATCTGAGATGTTATTTATGGGAGTTTCGAACCTTAA	1216
Db	1549	TTTACGATGGGTGGGAACAGTTATTCGCTGTGTACTTCTTGTGTGAAGACCTCA	1608
QY	1217	TTACCATTGGTGGCTTTCAGAAACCAAACTTTATTTGAAATGTTTTTCAACTCTTGA	1276
Db	1609	TCACCATGGGGGCTCCCTGACCCCAAGACACTCTTTGAAATTTGCTTCCAGCTGTCTGA	1668
QY	1277	ATTTTTTTCTGAGATTTTTGTGTTCTCCAGTTTTAAATTTGTGTGATGATGATGATG	1336
Db	1669	ATTATTTTCAGGGCGTCTTTGCTTTCTCTGTGATGATCGGACGATGAGAGATGTGGTAG	1728
QY	1337	GAGCAGCTACAGCCAATCAGAACTACTTTCGGCGCTCATGGATGACACCAATTCCTACA	1396
Db	1729	GGGCGGCCACCGGGGACAGACCTACTACCGCAGCTGCATGGACAGCACGGTGAAGTACA	1788
QY	1397	TGAACAAATTACTCCATTCCTAAACTTTGTGCAAAAGCGAGTTTCGAGCTTGATGAAATATA	1456
Db	1789	TGAATTTCTACAAGTCCCAAGTCCGTCAGAAACCCGCTCAAGACCTGGTACGAGTACA	1848
QY	1457	CATGGGACTCTCAAGAACTGATAGTAGTCTGATTTGCTTAAGACCTTACCAACTACGG	1516
Db	1849	CCTGGCACTCGCAAGGCATGCTGGATGAGTCAGAGCTGATGGTGCAGCTTCAGACAAGA	1908
QY	1517	TCAGATTAGCCCTCGCCATTGATGTGAACTTTCAGCATCATCAGCAAAAGTCGACTTTTCA	1578
Db	1909	TGCGGTGGACCTCGCCATCGACGTGAATACACATCGTTAGCAAAAGTCGACTCTTTC	1966
QY	1577	AGGTTGTGTATACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATT	1633
Db	1969	AGGCTGTGACCGGCAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTGCTTACC	2022
QY	1637	TGCTGTGTGACTTTGTCTGCAAAAGGGAGAAATTTGGCAAGAAATGTATATCATCAAGC	1699
Db	2029	TGCCCAACGACTATGTGTGCAAGAAAGGGGAGATCGGCGGTGAGATGTACATCATCCAGG	2088
QY	1697	ATGAGAAAGTCCAAAGTTCTTTGGAGCCCTGATGTGATATAAAGTTCTGTGTTACTGAAAG	1755
Db	2089	CAGGCAAGTGCAGGTCTTGGGCGCCCTGATGGGAAATCTGTGCTGTGTCAGCTGAAAG	2144
QY	1757	CTGGTTCGGTGTGGAAGAAATCAGCCCTTTAGCAGCAGGAGGAGGAACCGTCGAACTG	1811
Db	2149	CTGGATCTGTGTTTGGAGAAATAAGCTTGTGCTGTTTGGGGGGGGGAACCGGCCACCG	2200
QY	1817	CCAAATGTTGGGCCCAAGGTTTCCCAATCTTTAACTTAGACAAAGAACCCCTCCCAAG	1871
Db	2209	CCAAGTGTGGCGCACGGGTTTACCAACCTCTTCATCTCGATAAAGAGACCTGAATG	2266
QY	1877	AAATTCATGTCATATTCAGATTTCTGAAAGGATCTCATGAGAAACCGAGATGCTTTC	1933
Db	2269	AGATTTTGGTCATTATCTTGAAGTTTACTCCGGAAGAAAGCCAGGCGCATGC	2322
QY	1937	TAAAGCAGAGGCTTAAGACCGCAGAAG	1963
Db	2329	TGAGAGCAACAATTAAGCCCAAGGAGG	2355
RESULT 7			
LOCUS	HSU58837	4033 bp	mRNA
DEFINITION	Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.		linear PRI 18-JUL-1999
ACCESSION	U58837		
VERSION	U58837.1		
KEYWORDS	GI:1518638		

RESULT	7
HSU58837	
LOCUS	4033 bp
DEFINITION	Human CGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.
ACCESSION	U58837
VERSION	U58837.1
KEYWORDS	GI:1518638
PRI	18-JUL-1997
linear	mRNA


```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     1 (bases 1 to 930)
            Ardell,M.D., Makhlaja,A.K., Oliveira,L., Miniou,P.,
            Viegas-Pequignot,E. and Pittler,S.J.
TITLE       cDNA, gene structure, and chromosomal localization of human GAR1
            (CNGC31), a homolog of the third subunit of bovine photoreceptor
            cGMP-gated channel
JOURNAL     Genomics 28 (1), 32-38 (1995)
MEDLINE     96070429
PUBMED      7590744
REFERENCE   2 (bases 1 to 4033)
AUTHORS     Ardell,M.D., Aragon,I., Oliveira,L., Porche,G.E., Burke,E. and
            Pittler,S.J.
TITLE       The beta subunit of human rod photoreceptor cGMP-gated cation
            channel is generated from a complex transcription unit
JOURNAL     FEBS Lett. 389 (2), 213-218 (1996)
MEDLINE     96338110
PUBMED      8766832
REFERENCE   3 (bases 1 to 4033)
AUTHORS     Pittler,S.J.
TITLE       Direct Submission
            Submitted (20-MAY-1996) Pittler S. J., Department of Biochemistry
            and Molecular Biology, University of South Alabama College of
            Medicine, 307 University Blvd, Mobile, AL 36688-0002,USA
            Location/Qualifiers
FEATURES    source
            1..4033
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /chromosome="16"
            /map="16q13"
            /clone="hcc2"
            /cell_type="rod photoreceptor"
            /tissue_type="retina"
            /dev_stage="adult"
            1..4033
            /gene="CNGC2"
            1..57
            /gene="CNGC2"
            58..3813
            /gene="CNGC2"
            /function="modulation of channel activity"
            /codon_start=1
            /evidence=experimental
            /product="cGMP-gated cation channel beta subunit"
            /protein_id="AAB61387.1"
            /db_xref="GI:1518639"
            /translation="MLGVORVLPPPGTFRKTKMQEEVEPEPEMAEVEPEPEPNE
            EAETESSMPPEESFKEEVEVAVADPSPOETKEAALTSISLRQAQAEISMNPSHRY
            LTMKGVERVLPQPVSHVITEDPAQILHGSTGDTGCTDEPNEALRAQETRPLRLLL
            WLEQNLJRVLPQPKSVEWRDEPAVATGAASDPAPGRPOEMGPKLQARETSPLTP
            IPLQPKPEKAPAEPEPGSQAOQTSLSLPPTRDPAVLAWLHRLMALPOPLVHGKI
            GEQPDSPGLCDVQTSILPGGOVEPDLVLEVEPEPEWEDAHQVSTPOGTEVPVAYE
            EENKAVKMPRELRIEEXEEDDEEEEEEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVE
            DGTQPSTQDQMEVEGEAKAEAEKAEAEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVE
            ABAASSVPATKQHEPVQVEDTADSCPLMAENPPSTVLPPSPAKSDTLVPPSSAS
            GTRKLLPDEDEAEELKALSPAESPVVWSDPTTPKTDQDRAASTASTNSAIND
            RLQVLKLFKFRKTKVKELIDPDVTSDESPKSPAKAPAPAPDTKPAEAPVPEE
            HYCDMLCKFKRHWKVKYQFQSDIDPLTNLMVYLWLFVVMWNNWNLIPVRWAPPY
            QTPNTHLLMLDLVCLDILVFLDITVPTQLQVRGDIITDKDKNNYLKSRFKM
            DLSSLPLDLKLVGVNPLRLPRCLKNYAFEPNRSLESILSKAYVVRVIRTAYL
            LYSLHNSLYYNWASVQGLGTHWDVGNSTIRICYPFAVKILITIGLDPDKFL
            EIVFQLNLYTFVAFSVMLGQMRDVVGAATAGOTYRSCMDSTVKYMPFKIPKSVQ
            NRKVTYETWGSQDMEBELVQPLDRLDAIDVNNIVSKVLFQGCDDRMIF
            DMLKRLSVVLYFNDDYCKKEIGREMYIIQAGOVVLGPDGKSVLTKAGSVFGE
            ISLIAVGGGNRRNTANVVAHGFTNLFILDKDLNEILVHPESQKLKRRKARMLRNN
            KPKEKSVLILPRAGTPKLPNALAMTGMKGKAGKGLAHLARLKLALALEAA
            KHELVEQAKSSODVKEEGSAAPDOHTHPKEATDPAPRTPPEPGSPSPPPAS
            LGSCEBEEGPAPPEHSVRLCMSPGPEFQELISVMPEEREKAE"
            58..2851
            misc_feature

```


QY	1397	TGAACAAATTACTCATTTCCATAACTTGTGCACAAAGCGAGTTCGGACTTGGTATGAATATA	1456
Db	2768	TGAATTTCTAAAGATCCCAAGTCCGTGCAGAACCGGCTCAAGACTGGTACGACTACA	2827
QY	1457	CATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAAGACCCCTACCAACTACGG	1516
Db	2828	CCTGGCACTCGCAAGGCATCTCGATGAGTCAGAGCTGATGGTGCAGCTTCACAGACAAGA	2887
QY	1517	TCAGATTAGCCCTCGCCATTGATGTGAACCTCAGCAATCATCAGCAAGTCGACTTCTTCA	1576
Db	2888	TGGGCTGGACCTCGCCATCGAGCTGAACCTACCAACATCGTTGCAAGTCGCACTCTTTC	2947
QY	1577	AGGCTTGTGATACACAGATGATTTATGACATGTTGCTTAAGATTGAAATCGTTCTCTATT	1636
Db	2948	AGGCTGTGACCGGCAGATGATCTTTGACATGCTGAAGAGCTTCGCTCTGTTGTCTAGC	3007
QY	1637	TGCTGTGTGATCTTGTCTGAAAGAGGAGAAATTCGCAAGGAAATGATATATCATCAAG	1696
Db	3008	TGCCCAACGACTATGTGTGCAAGAGGGGAGATCGCGCTGAGATGTACATCATCAG	3067
QY	1697	ATGAGAGAGTCCAAGTTCTTTGGAGGCCCTGATGTAAGTTCTGGTTACTCTGAAAG	1756
Db	3068	CAGGCAAGTGCAGTCTTGGCGGCCCTGATGGGAAATCTGTGCTGGTACGCTGAAG	3127
QY	1757	CTGGTCTGGTGTGGGAGAAATCAGCCCTTCTAGCAGCAGAGAGGAAACCGTCTGAAC	1816
Db	3128	CTGGATCTGTGTTGGAGAAATAAGCTTGTGCTGTGGGGCGGGAACCGCGCACCG	3187
QY	1817	CCATGTGTGGCCCGCCGCTTGCCTTCTTAACTCTAGACAAAGACCCCTCCAAG	1876
Db	3188	CCAACGTGGTGGCGCAGCGGTTTACCAACTCTTCTCTGGATAGAGACTGATAG	3247
QY	1877	AAATTTAGTGCAATATCCAGATTCTGAAAGGATCTTCATGAAGAACCGAGTCTTT	1936
Db	3248	AGATTTGGTGCAATATCTCTGAGTCTCAGAAGTTACTTCGGAAGAACCGAGCGCATG	3307
QY	1937	TAAGCAGAGGCTAAGACCCAGAAG	1963
Db	3308	TGAGAGCAACAATAAGCCCAAGGAG	3334
RESULT 8			
LOCUS	AF042498	4382 bp	mRNA linear PRI 02-MAR-1998
DEFINITION	Homo sapiens rod photoreceptor CNG-channel beta subunit (RCNC2)		
ACCESSION	AF042498	mRNA, complete cds.	
VERSION	AF042498.1	GI:2921582	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 4382)		
TITLE	Grunwald,M.E., Yu,W.P., Yu,H.H. and Yau,K.W.		
JOURNAL	Identification of a domain on the beta subunit of the rod		
REFERENCE	cGMP-gated cation channel that mediates inhibition by		
AUTHORS	calcium-calmodulin		
TITLE	J. Biol. Chem. (1998) In press		
JOURNAL	2 (bases 1 to 4382)		
REFERENCE	Grunwald,M.E., Yu,W.P., Yu,H.H. and Yau,K.W.		
AUTHORS	Direct Submission		
TITLE	Submitted (12-JAN-1998) Neuroscience, Johns Hopkins University		
JOURNAL	School of Medicine, 725 N. Wolfe St., Baltimore, MD 21205, USA		
FEATURES	Location/Qualifiers		
source	1..4382		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
gene	1..4382		
	/gene="RCNC2"		
CDS	71..3808		
	/gene="RCNC2"		

/note="cyclic nucleotide-gated cation channel beta subunit"			
/codon_start=1			
/product="rod photoreceptor CNG-channel beta subunit"			
/protein_id="AAC04830.1"			
/db_xref="GI:2921582"			
/translation="MLGWQVRLVPQPPGTPRKTKQEEVEPEPEAEVEPEPNPE			
EAETSESPPEEVEEVAADVPQETKEAALTSTISRAQGAISENPSHRV			
LTMKGVKVIPOVHSITEDPAQILHGSTGDTGDTDFNEALEAQDTPRL			
WLEONRLVPPPKSEVWEDEPAVATPPRQEMGPKLQARETSLPTPI			
BEPEAPAPPOGSOQATSLPTRPDLAVLHRLMALPQVLHGKIQEOPD			
SPGCDVDTISILFGQVPEPLVLEVEPEWEDAHQDVSPQTEVVPVPEENKAV			
EKMRSEURIEEKEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEE			
STSQKWEVEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE			
GVPAKQHPVEQVEDTDADSCPLMAEENPPSTVLPPSPAKSDTLI			
LPSDDEAEELKALSPAESPVAWSDPTTKDQDQRAASTASNGAI			
CKFKERPKVKEKILDPDVTDESPKSPAKKAPAPDPAEAPVEBEHYCDML			
HMLMDYLCILITFDLITVQTRQLQVRGGDIITDKDMRNVLKSRFRKMDL			
PDLFLYKVGVPRLRPLRCLKYNAPFENFNRLESILSKATVYRIVRTYLLSLHL			
NSCLYASAYQGLSTHWYGVNSYIRCYFAVTLITIGLPPDPTLFI			
LNYETGVPAFVMIGQMDVYGAATAGTYYRSCMDSTVKYMFYKIP			
YEYTHSQMDLDESELVQLPDKVRLDLAIQVNYINIVSKVAFQCCDQ			
RSVYLPNDYVCKGEIGREMYIIQAGOVVLGGPDGKSLVTLKAGSVGEI			
CGHRRTANVVAHGTNLFLDKDLNAILVHYPESOKLRLKARRMLKSR			
SVLILPPRAGTPTKFNALAMTGMKGKAGKGLAHLRLKELAALEAAKQ			
POAKSQDVKGEGSAAPDQHTHPKBAATPPAPTPPEPPGSPSPSP			
BEEGPAEPEEHSVRICMSPGPEGEQLSVKXNPEEBKAE"			
ORIGIN			
Query Match 23.8%; Score 577.4; DB 9; Length 4382;			
Best Local Similarity 64.3%; Pred. No. 5.9e-101; Indels 0; Gaps 0;			
Matches 866; Conservative 0; Mismatches 481;			
QY	617	TTCCAAAACAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTCTTGGTGTGCA	676
Db	1983	TTCCCCAGAGCATTCACCGCTGACCAACCTGATGTATGCTATGCTTCTTCGTGG	2042
QY	677	CTCTTGGCTATAACTGGAACTCTGTTTATACCACTGGCTCTCTTCCCATATCAA	736
Db	2043	TGATGGCTTGGAAATGGAACTGTTCGGCTGATTCGGCTGGGCGCTTCCCTACCA	2102
QY	737	CGCAGACAAACATACACTACTGGCTTATTCGGGACATCATATGTATCATCTACCTT	796
Db	2103	CCCCGACAACTCCACCTGCTGCTGATGATTACCTATGCGACCTCATCTACTCC	2162
QY	797	ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAGAGGAGAGACATAAGTGG	856
Db	2163	TGSACATACCCGTGTTCCAGACACGCTGCGAGTTTGTTCAGAGCGGGGACATACGG	2222
QY	857	ATTCAAATGAGCTAAGGAAACACTACAGACTTCTACAAAATTTTCAGTTGGATGCGCAT	916
Db	2223	ACAAAAGGACATGCGAAATACTACCTGAGTCTCGCGCTTCAAGATGGACCTGCTCA	2282
QY	917	CAATAATACCATTTGATATTTGCTACCTCTCTTTGGTGTAAATCCATGTTTAGACAA	976
Db	2283	GCCTCTGCTGCTTGGATTTCTTATTTGAAAGTCGGTGTGAACCCCTCTCCCGCTGC	2342
QY	977	ATAGGATGTTAAGTACACTTCTATTTTGAATTAATCATCACCTAGAGTCTATAATGG	1036
Db	2343	COGCTGTTTAAAGTACATGGGCTTCTTCGAGTTTAAAGCGCGCTGGAATTCATCTCA	2402
QY	1037	ACAAAGCATATATCTACAGAGTTTATTCGAACAACTGGATACCTTGTGTTTATTTCACA	1096
Db	2403	GCBAAGCCTACGTGTACAGGGTCAACAGGACACAGCCTACCTTCTTACAGCCTGCA	2462
QY	1097	TTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAGGAATGGCATCTAGATGG	1156
Db	2463	TGAATTCCTGCTCTTATTACTGGGCATCGGCTATCAGGCGCTCGGCTCCACTCTAGT	2522
QY	1157	TGTATGATGGGAAGGAAACGAGTATCTGAGATGTTTATTATTTGGGAGTTCGAACCTTAA	1216
Db	2523	TTTACGATGGCGTGGGAAACAGTTATTTGCTGTTTACTTACTTGTGCTGAGACCTCA	2582


```

GSDIITDKKEMRNLYKSRFRMDLLCLPLDLYLKLGINPLRLPRCLKMAFPF
NNLEIAIKAVYVIRTYLAILSLNSCLYVWASAFQIGSTHWYDVGNSYI
RCYVAVKLTITGGLPDPTLFEIVQLLNYFTGFVAFSVIMIGOMRDVGAATAGOT
YVRSMDSTVKYMNFKI PRSQNRVKTWYETVHSOGLDESLMVLDPKRLDILA
IDVNSVSKVALFOGCDQMLFDMKRLRSVYLPNDVCKKGBIGREMYIOAGOV
QVLGGPDGRVAVTLKAGSVFGEISLLAVGGNRPRTANVAVHGFNLFILDKKDLNEI
LVHPSQMLRLKRRMLRNKPKESVILILEPRAGTPKLFNVALAAGKMGPRG
AKGKLALRLKLEALALEAARQOQLLEQAKSOEAGEEGSGATDOPAPQEPPEP
KDPKPPGPPPSAQSPPPASAPKPESTGEAAGPPSPSVIRVSPGPDGSGQTLVSE
VLBEKEGAE"
misc_feature
920..1489
/ gene="Cngb1"
/ note="ion_trans; Region: Ion transport protein. This
family contains Sodium, Potassium, Calcium ion channels.
This family is 6 transmembrane helices in which the last
two helices flank a loop which determines ion selectivity.
In some sub-families (e.g. Na channels) the domain is
repeated four times, whereas in others (e.g. K channels)
the protein forms as a tetramer in the membrane. A
bacterial structure of the protein is known for the last
two helices but is not the Pfam family due to it lacking
the first four helices"
/ db_xref="CDD:pfam00520"
/ db_xref="CDD:pfam00520"
misc_feature
1784..2065
/ gene="Cngb1"
/ note="cNMP_binding; Region: Cyclic nucleotide-binding
domain"
/ db_xref="CDD:pfam00027"
ORIGIN
Query Match 23.7%; Score 575.2; DB 10; Length 4763;
Best Local Similarity 63.6%; Pred. No. 1.5e-100;
Matches 915; Conservative 0; Mismatches 508; Indels 15; Gaps 2;
617 TTCCAAACAGCATAGATTCATACACAGATCGACTCTATCTCTCTGTGGCTTCCTGTGCA 676
783 TCCCCAGAGATCGACCCACTGACCAACCTCATGTACATCTTGTGGCTCTTCTTTGTGG 842
677 CTCTTGCTTAATCGTGAATGCTGTTTATACACACTGCGCCTCGTCTCCCATATCAAA 736
843 TGCTGGGCTGGAAGTGGTGGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
737 CCGCAGACACATACACTACTGCTTATGCGGACATCATATGATATCATCTACTCTTT 796
903 GGGCAGACACATCCACTTCTGGCTCTCATGATGATTTCTGTGCGACTTCTATCTACCT 962
797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAGAGGAGGAGACATATAGTGG 856
963 TGSACATACCGTGTTCAGATGCGCTGCGAGTTTGCAAGGCGGGGACATCATACAG 1022
857 ATTCAATGAGCTAAGAAACACATACAGGACTTCTACAAAATTTTCAGTTGGATGTCG 916
1023 ACAAGAGGAGATCGGTATTAATCTACCTGAAGTCTCGCGGTTTAAAGATGGACCTGCT 1082
917 CAATAATACCAATTTGATTTGCTACCTCTCTTTGGTGTATCCAAATGTTAGACAA 976
1083 GCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1142
977 ATAGATGTTAAAGTACATCTTCTTTTGAATTAATCATCACTAGACTAGTCTATAATGG 1036
1143 CCGCTGCTGAGATGATGCTTCTTCTTGTGATTTAATACCGCTGGAAGCCATCTCA 1202
1037 ACAAGCATATATCTACAGATTTATCGAACAACTGGATATCTGCTGTTTATCTGCACA 1096
1203 GCAAAGCCTACGTTTACAGAGTCATCAGAACCGGCTTACTGCTGTACAGCTGCGACC 1262
1097 TTAATGCTGCTGTTTATTTACTGGCTTCAAACTATGAGGAATTTGGCACTAGATGGG 1156
1263 TCAACTCTGCTTTTACTTACTGGGATCAGCCTTCCAGGGATCGCTTCCACTCAGTGG 1322
1157 TGTATGATGGGAGAAACGAGTATCTGAGATGTTATTTATGGCGAGTTCGAACTTAA 1216
1323 TTACAGCGAGTGGGACAGTTATATTCGATGCTACTTCTGCGCTGTGAAACCCCTCA 1382

```

```

QY 1217 TTACATTTGGTGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTCAACTCTTGA 1276
DB 1383 TCACCATCGGAGGACTGCGCCACCCAGACGCTCTTTGAGATTTGTTTCCAGTCTGTA 1442
QY 1277 ATTTTCTTCTGAGTTTCTTGTGTTCTCCAGTTTAAATTTGTTTCAAGATGATGATTG 1336
DB 1443 ACTATTTACCGGGGTCTTTGCTTCTCTGTGATGATTTGGACAGATGAGAGATGTTG 1502
QY 1337 GAGCAGCTACAGCCAAATCAGAACTACTTCCCGGCTGATGATGATGACACCAATTCGCTTACA 1396
DB 1503 GGGCGCCACACAGCGGGGAGACCTACTACCGCAGCTGATGAGCAGCAGCAGTGAAGTACA 1562
QY 1397 TGAACAATTTACTCCATTTCTTAACTTTGTGCAAAAGCGAGTTCCGACTTTGGTATGAATATA 1456
DB 1563 TGAATTTCTACAGATCCCGAGTCTGTGAGACCGGTGTCAAGACCTGTTGATGATGATACA 1622
QY 1457 CATGGACTCTCAAGAAATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1516
DB 1623 CTGGCAATTCGCAAGGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1682
QY 1517 TCCAGTTAGCCCTCGCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1576
DB 1683 TCGCACTGGACTGGCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1742
QY 1577 AGGGTTGTGATACACAGATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1636
DB 1743 AGGGCTGTGACCGGAGATGATTTCTGACATGCTCAAGCGGCTTCTGTTCTGTCTACC 1802
QY 1637 TGCCTGTGACTTTGTCTGCAAAAGGAGAAATTTGGCAAGGAATGATATATCATCAAGC 1696
DB 1803 TACCCAATGACTATGTGTGCAAGAGGGGAGATTTGGCCGAGAGATGATACATTTATCCAG 1862
QY 1697 ATGGAGAGATGCTCAAGTCTTGGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 1756
DB 1863 CCGGCGAGTGTGAGTGTGCTGGCGGCCAGATGGAAGGCTGTACTGTGTGACACTCAAG 1922
QY 1757 CTGGTGTGCTGTTGGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCGTCCAACTG 1816
DB 1923 CCGGATCGGTGTTGGAGAAATTAAGCTTGTCTGGCTGTCTGGGGGTGGCAACCGCGGCACAG 1982
QY 1817 CCAATGTGTGGCCACCGGTTTGCCTTCTTTAACTCTAGACAAAAGACCTTCCCAAG 1876
DB 1983 CCAAGGTGTGGCCATGCTTCTTCAACCTTCTTCACTGTGACAGAGGACTTTGAATG 2042
QY 1877 AAATTTCTAGTCAATTTCCAGATTTCTGAAGGATCTCATGAAGAAAGCCAGAGTGTCTTT 1936
DB 2043 AAATTTCTAGTCAATTTCCAGATTTCTGAAGGATCTCATGAAGAAAGCCAGAGTGTCTTT 2092
QY 1937 TAAAGCAGAGCTTAAGACCGCAGAGCAACCCCTCCAGAAAGATCTTGCCTCTCTCT 1996
DB 2093 ---AGCGCATGCTTAAGAAATTAACAAACCCCAAGGAGGAAAGA--GTGTCTCATCC 2147
QY 1997 TCCACCGGAAAGAGACACCCAACTGTTTAAAACTCTCTAGAGGACAGGAAA 2054
DB 2148 TGCCCCCGCTGGGGCACCCCGAGCTCTTCAATGCTGCCCTGGCTGTGAGGAAA 2205

```

```

RESULT 10
AF074012 3083 bp mRNA linear MAM 30-OCT-2001
LOCUS
DEFINITION
Bos taurus cyclic nucleotide-gated channel beta subunit 1c
(CNCheta) mRNA, complete cds.
ACCESSION
AF074012
VERSION
AF074012.1 GI:3309621
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 3083)
REFERENCE
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and
AUTHORS

```


AF074013	QY	857	ATTCAATAGCTAAGGAAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCGAT	916
AF074013.1	Db	1186	ACAAAAAGGAGATGCGCAAAATTTACGTGAATCTCAGCGCTTTAAGATGACATGCTCT	1245
Bos taurus (cow)	QY	917	CAATAATACCAATTTGATATTTGCTACCTCTTTTGGGTTTAATCCAAATGTTTAGACAA	976
Bos taurus	Db	1246	GCCTCTGGCCCTTGAGACTTACTCTGAAATTCGGTGTGAATCCCTCTCTGGCTGTC	1305
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	QY	977	ATAGATGTTAAAGTACACCTTCATTTTGAATTTAATCATCACTAGAGTCTAATAGG	1036
1 (bases 1 to 3090)	Db	1306	CCCGCTGTTTGAAGTATATGCGCTTCTTTGAGTTTAAACCGCTGGAATCCATCTCA	1365
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and Weyand,I.	QY	1037	ACAAAGCATATATACAGAGTATTGAAACAACTGGATCTCTCTGTTTATTTCTGCACA	1096
Cyclic nucleotide-gated channels on the flagellum control Ca2+ entry into sperm	Db	1366	GAAAGCCTTACGTTTACAGGTTTATCAGACACAGCTACTCTCTACAGCTTACATC	1425
J. Cell Biol. 142 (2), 473-484 (1998)	QY	1097	TTAATGCTCTGTTTATTACTGGCTTCAAACTAAGAAATTTGGCACTACTAGATGGG	1156
98345361	Db	1426	TGAACCTCATGCTCTATTACTGGGCTCGGCTATGAGGCTCGGCTCCACTCCTGGG	1485
9679145	QY	1157	TGATGATGGGGAAGAAACGAGTATCTGAGATGTTATTATTGGGAGTTCGAACTTAA	1216
2 (bases 1 to 3090)	Db	1486	TTTATGATGGGCTGGGAAACAGTTACATTCGCTGTTACTCTGGCTGTGAAGCCCTCA	1545
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and Weyand,I.	QY	1217	TTACCAATGGTGGCTTCCAGAAACCAAACTTTTATTGAAATTTGTTTCAACTCTTGA	1276
Direct Submission	Db	1546	TCACCATCGCGGCTGCCGACCCAGGACGCTCTTTGAAATTTGCTTCCAGGCTCAA	1605
Submitted (24-JUN-1998) FBI, FZ-Juelich, Leo-Brandt-Strasse, Juelich, NRW 52425, Germany	QY	1277	ATTTTCTTGGAGTTTGTGTTTCTCCAGTTTAAATTTGCTCAGATGAGAGATGATTG	1336
Location/Qualifiers	Db	1606	ACTATTTTCAAGGCTCTCTCGCTTTCTCGGTGATGATCGGACAGATGAGACGATG	1665
1..3090	QY	1337	GAGCAGCTACGCCAATCAGAACTACTTCCGCGCTCGATGGATGATGACACCACTTGC	1396
/organism="Bos taurus"	Db	1666	GGCGCCGACCCGCGGACAGACCTACTACCGAGCTGATGATGACGACGACCGTGAAGTATA	1725
/mol_type="mRNA"	QY	1397	TGAACAAATTTACTCCATTTCTAAATTTGTGCAAAACGAGTTCCGAGTTGGTATGAATA	1456
/db_xref="taxon:9913"	Db	1726	TGAACCTTCTACAAATCTCCAGTCCGTCGAGAACCGGCTCAAGACCTGGTACGAATA	1785
1..3090	QY	1457	CATGGAGCTCTCAAGAAATGCTAGATGATGCTGATTGCTTAAAGACCTTACCAACTAGG	1516
/gene="CNCbeta"	Db	1786	CTGGGACTTCCCAAGGATGCTGGATGATGATGATGATGATGATGATGATGATGATG	1845
12..2858	QY	1517	TCCAGTTAGCCCTCGCAATTTGATGTAATTCAGCATCATCAGCAAAAGTCTGTTTCA	1576
/codon_start	Db	1846	TGCGGCTGGAACCTCGCAATTTGATGTAATTCAGCATCATCAGCAAAAGTCTGTTTCA	1905
/product="cyclic nucleotide-gated channel beta subunit 1d"	QY	1577	AGGTTTGTGATACAGATGATTTATGATGATTTGCTTAAGATTTGAAATCCGTTCTCTATT	1636
/protein_id="AAC26128.1"	Db	1906	AGGCTGTGACCGGCGATGATCTTTGATGATGATGATGATGATGATGATGATGATG	1965
/db_xref="GI:3309624"	QY	1637	TGCTGCTGCTGCTTTGCTCAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC	1696
/translation="MDACGGDAQTAGCLSGVSHVLLDSYLPQSEEDRSESETQD	Db	1966	TGCCCCAATGATGCTGTGTCAGAGAGAGGAGATAGGCGCGGAAATGTATCATCATCAGG	2025
OSVGAQAQGEVGAQAQALSESETQDQSEVGAQAQSEVGAQAQSEVGAQAQSEVGAQAQSEV	QY	1697	ATCGAAGATGCTCAAGTTCTTGGAGGCTGATGATGATGATGATGATGATGATGATG	1756
GGADQSTQGEVGAQAQALADSEVGAQAQSEVGAQAQSEVGAQAQSEVGAQAQSEVGAQAQ	Db	2026	CGSGGAGATGCTCAAGTTCTTGGTGGGCTCGGATGGAATTCGCTGCTGGTGAAGG	2085
LSAKSTLAVGSATGSLKRLPSODDEAEELKMLSPASPVVANSDDTSPGOTDQ	QY	1757	CTGGGCTGGTGTGGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCGTCTGAAGT	1816
DRATSTASQNSALINDKQLVLKFKERTKVKELDPDVTDESPKPKAKPE	Db	2086	CTGGAATCTGTGTTTGGAGAAATTAAGTTGCTGGCTGTAGGGGCGGGAACCGCGCACAG	2145
PAPEVPAEAGVVEEHCEMLCKFKRPPKWKIPQPSIDPLTNLYMLILNLFVFLA	QY	1817	CCAATGCTGGTGGCCCGGCTTTCGAAATCTTTTAACTCTAGACAAAAGACCTCTCAAG	1876
WNWMLIPVMAFPYPTPDNIHLWLLMDYLCDLILYLLDITVFMRLQFVRGGDILTD	Db	2146	CTAACGTTGGTGGCCCATGCGTGTACCAACCTCTTCTTCTTCTTCTTCTTCTTCTTCT	2205
KKMNRYVKSQFPMQMLCLLPLDLLYLFKFGVNLRLPRCLKYNAFFENRLRSL	QY	1877	AAATTTCTAGTGCATTCAGATTTCTGAAGGATCTCTCATGAAGAAGCCAGAGTGTIT	1936
LSKAVVYVIRTTAYLLSLNLSLYWASVEGLSTHWVGVGNSVIRCYWAV	Db	2206	AAATTTCTGGTGCATTTATCCGAGTCTCAGAAAGTTGTTCCGCAAGAGCCGCGATGC	2265
KTLLTIGLDPDPTLFIIFQGLNFTGTFVAFSVMIQMDRVVGAATAGOTVYRSQMD	QY	617	TTCCAAACAGATAGATTTCACACAGATCGACTCTCTCTCTGCTGCTGCTGCTGCTCA	676
STVKMNFYKIPSVQNRVNTVYVTHWSQMDSESLVQLPKMRLLDLAI DVNYSI	Db	946	TTCCCAAGAGATGACCGCTGACCAACCTGATGATGATGATGATGATGATGATGATG	1005
VSKVALFGQDQRQIMFQMLKRLSVVLPNDYVCKGEIGREMYIIQAGOVVLGPD	QY	677	CTCTTGGCTATAACTGGAACCTGCTGTTTATACCACTCGCTCGCTCTCTCTCTCTCT	736
QKLLRKARRMLRNPKKSVLILPFRAGTPKLFNALAAAGKMGKAGGGRGLAL	Db	1006	TGCTGGCTTGGAACTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1065
LRALKELAALEAAQQQLLEQAKSDEDAVGEESASPEQPPPEPPAPAPAPAP	QY	737	CGGAGACAAATACACTACTGGCTTATGGGACATCATATGTCATCATCATCATCTT	796
TAPELAPAPAPAPAPAPSPPPASQERPEGDKDAARPEHPVRIHVTLGPDPEQIL	Db	1066	CGCCAGACAAATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1125
LVEVPEKQSEKEKEEETBEKEGEARKEEE"	QY	797	ATGATATGCTATTATTCAGCCCACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTG	856
	Db	1126	TGGACATCACCGTGTTCAGATGCGCTGCGAGTTTGTTCAGAGGGGGGACATCATCGG	1185

ORIGIN

Query Match	23.5%	Score 572.2;	DB 4;	Length 3090;
Best Local Similarity	64.1%	Pred. No. 6.1e-100;		
Matches 862;	Conservative 0;	Mismatches 483;	Indels 0;	Gaps 0;
yy	617	TTCCAAACAGCATAGATTTCATACACAGATCGCACTCTATCTCTCTGCTGCTTGTGCTTCA	676	
bb	946	TTCCCAAGAGCATCGACCGCTGACCAACCTGATGATCATCTTGTGGCTGTCTTCTGTGG	1005	
yy	677	CTCTTGGCTATAACTGGAACTGCTGGTTTATACCACTCGCGCTGCTTTCCTCATCAAA	736	
bb	1006	TGCTGGCTTGGAACTGGAACCTGCTGCTGANTCCCGCTGCGTGGGCTTTCCTCATCAGA	1065	
yy	737	CGCGACAGCAATACACTACTGGCTTATTCGGGACATCATATGTCATATCATCTACCTTT	796	
bb	1066	CGCCAGACAACTCCACCTCTGGCTGCTGATGGAATACCTGTGTGACCTCATCTACCTCC	1125	
yy	797	ATGATATGCTATTATTCAGCCCACTCCAGTTTGTAAAGAGGAGGACATATATGTGG	856	
bb	1126	TGGACATCACCGTGTTCAGATGCGCTGCACTTGTTCAGAGGGGGACATCATACGG	1185	

ACCESSION AF074013
 VERSION AF074013.1
 KEYWORDS GI:3309623
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 3090)
 AUTHORS Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and Weyand,I.
 TITLE Cyclic nucleotide-gated channels on the flagellum control Ca2+ entry into sperm
 JOURNAL J. Cell Biol. 142 (2), 473-484 (1998)
 MEDLINE 98345361
 PUBMED 9679145
 REFERENCE 2 (bases 1 to 3090)
 AUTHORS Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and Weyand,I.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-1998) FBI, FZ-Juelich, Leo-Brandt-Strasse, Juelich, NRW 52425, Germany
 FEATURES
 source
 gene
 CDS

1919 AGGGCTGTGACCGGAGATGATCTTTGACATGCTGAAGAGGCTGCGCTCTGTAGTCTACC 1978
1637 TGCTGTGATCTTTGCTGCAAAAGGAGAAATGGCGAGGAATGTATATCATCAGC 1696
1979 TGCCCAATGATTAAGTGTGCAAGAGGAGGAGATAGCGCGGAAATGTATATCATCAGC 2038
1697 ATGGAGAGTCCAAAGTCTTGTGAGGCGCTGATGCTTAAGATCTTGTGTTACTCTGAAG 1756
2039 CGGGGAGGTGAGGCTTGTGGTGGCGCGGATGGGAATCCGCTGCTGTGAGCGTGAAG 2098
1757 CTGGTGGGTGTTTGGAGAAATCAGCTCTTACGACGAGAGGAGAAACCGTGAAGT 1816
2099 CTGGATCTGTGTTGCGAGAAATAGCTTGTGCTGTAGGGGCGGAAACCGGCGCAG 2158
1817 CCAATGTTGGGCGCGGCTTGGCAATCTTTTAACTCTAGACAAAAGACCTCCAAG 1876
2159 CTACGTTGGTGGCGGCTTGGCAATCTTTTAACTCTAGACAAAAGACCTCCAAG 2218
1877 AAATTTCTAGTGCATTTCCAGATTTCTGAAAGTCTTCTGAAAGTCTTCTGAAAG 1936
2219 AAATTTCTAGTGCATTTCCAGATTTCTGAAAGTCTTCTGAAAGTCTTCTGAAAG 2278
1937 TAAAGCAAGAGGTGAGACCGCAGA 1961
2279 TGAGAAATTAACAAGCCCAAGGA 2303

RESULT 13
AF074014 3290 bp mRNA linear MM 30-OCT-2001
LOCUS Bos taurus cyclic nucleotide-gated channel beta subunit 1e
DEFINITION (NCBbeta) mRNA, complete cds.
ACCESSION AF074014
VERSION AF074014.1 GI:3309625
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 3290)
Wiesner, B., Weiner, J., Middelhoff, R., Hagen, V., Kaupp, U.B. and
Weyand, I.
Cyclic nucleotide-gated channels on the flagellum control Ca2+
entry into sperm
J. Cell Biol. 142 (2), 473-484 (1998)
98345361
9679145
2 (bases 1 to 3290)
Wiesner, B., Weiner, J., Middelhoff, R., Hagen, V., Kaupp, U.B. and
Weyand, I.
Direct Submission
Submitted (24-JUN-1998) IBI, PZ-Juelich, Leo-Brandt-Strasse,
Juelich, NRW 52425, Germany
Location/Qualifiers
1..3290
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
1..3290
/gene="NCBbeta"
200..3058
/gene="NCBbeta"
/codon_start=1
/product="cyclic nucleotide-gated channel beta subunit 1e"
/protein_id="AAC26129.1"
/db_xref="GI:3309625"

translation="MNVTAPLSGSCIMASLLAKTAPNHSVLLDSYLPQSEEDRSEES
ETQDSVGGACQGEVGAQALSEESTQDSVGGAAQDSVGGAAQGEVGGAGAE
QDVGGAQDSSTQGEELADSSGPATEHEPELQVEDADADSRPLTAENPPSP
VQLPSPKSTLAVPGATSLKRLPLSQDDEBELKMLSPASPVVMSDPTSPQ
TDDQRTATSTAVNIDRLQELVLFKERTKVKELIDPVTSDSESPKSPAK
KAPFAPKFAEAGQVEEHCYEMLOCKFKRPKPKKYPQPSIDPLINLMLLWLF

FEATURES
source
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
1..3290
/gene="NCBbeta"
200..3058
/gene="NCBbeta"
/codon_start=1
/product="cyclic nucleotide-gated channel beta subunit 1e"
/protein_id="AAC26129.1"
/db_xref="GI:3309625"

gene
CDS
1..3290
200..3058
/gene="NCBbeta"
/codon_start=1
/product="cyclic nucleotide-gated channel beta subunit 1e"
/protein_id="AAC26129.1"
/db_xref="GI:3309625"

translation="MNVTAPLSGSCIMASLLAKTAPNHSVLLDSYLPQSEEDRSEES
ETQDSVGGACQGEVGAQALSEESTQDSVGGAAQDSVGGAAQGEVGGAGAE
QDVGGAQDSSTQGEELADSSGPATEHEPELQVEDADADSRPLTAENPPSP
VQLPSPKSTLAVPGATSLKRLPLSQDDEBELKMLSPASPVVMSDPTSPQ
TDDQRTATSTAVNIDRLQELVLFKERTKVKELIDPVTSDSESPKSPAK
KAPFAPKFAEAGQVEEHCYEMLOCKFKRPKPKKYPQPSIDPLINLMLLWLF

VVLAWNNWNLIPVRWAFYQTPDNHILWMLDYLCDLIYLLDITVFMRLQFVRGSD
IITDKEMRNYYKSRFQMDLCLPLDLILYKFGVNLRLPRCLYKAFEFNNR
LESLIXAYVVRIRITAYLLYSLHNSCLLYWASAYEGLSGTEWYDVGNSYIRCY
YWAKTLLITIGLPLDRLTPEIFVQGLNYFTGFVAFSWMICQMDVVGATAGQTYR
SCMDSTVKNVFKYIPSVONRVKTYEYTHSQMLDESLMVLQPKRRLDLAIDV
NYSIVKVALFOGCDROMI EDMKRLSVLYLNDVYVCKKEIGREMYIIQAGOVOL
GPDGKSVLVLTKAGSVFGISLLAVGNNRRTANVVAHFTNLFLDKDLNELLVH
YPSQKLLRKARMLNNPKESVLIPLPRAGTPEKFNALAAAGKAGKAGRG
RLALRLARLEALAAEAARQQLEAKSEDAVGEBSAPSEPPRPPAPAP
APEPTAPEPLAPEAPAPSPSPASQERPEGDKDAARPEHPVRIIHTLUGDPDS
EQILLVVEPQEBKEKEBETEBKEBGEARKEKEE"

ORIGIN
Query Match 23.5%; Score 572.2; DB 4; Length 3290;
Best Local Similarity 64.1%; Pred. No. 6.1e-100;
Matches 862; Conservative 0; Mismatches 483; Indels 0; Gaps 0;
617 TTCCAAAACAGATGATTATACACAGATCGACTCTATCTCTCTGTGGCTCTTGTCTGCA 676
1146 TTCCCAAGAGATCGACCGCTGACCACTGATGATCATCTTGTGGCTGTCTTCGTGG 1205
677 CTCTTGGCTATACTGGAACCTGCTGTTTATACCACTCGCGCTCGTCTTCCCATATCAA 736
1206 TGCTGGCTGGAACCTGGAACCTGCTGCTGATTCGCTGCGCTGCGCTTCCCTATCAGA 1265
737 CGCGAGACATACACTACTGCTTATTGCGGACATCATATGATATCATCTACCTTT 796
1266 CGCCAGACAACATCCACTCTGGCTGTGATGATGATGATGATGATGATGATGATGAT 1325
797 ATGATATGATATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGAGACATAATAGTGG 856
1326 TGGACATCACCCTGTTCCAGATGCGCTGCACTTGTTCAGAGGCGGGGACATCATTCAGG 1385
857 ATTCAAATGAGTAAGGAAACACTACAGACTCTTACAAAATTTTCAGTTGATGTCGCAT 916
1386 ACAAAGAGAGATGCGCAACAAATTACGTGAATCTCAGCGCTTTAAGATGGAATGCTCT 1445
917 CAATAATACATTTGATATTTGCTACCTCTTCTTTGGTCTTAAATCCAATGTTTAGAGCAA 976
1446 GCCTCTTGGCTTGAATCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 1505
977 ATAGAGTGTAAAGTACATCTTCAATTTTGAATTTAATCATCATCTAGTGTCTATAATGG 1036
1506 CCGCTGTTTGAAGTATATGCGCTTCTTTGAGTTTAAACAACCGCTGGAATCCATCCTCA 1565
1037 ACAGACATATCTACAGAGTATTTCGAAACAACTGATCTTGTCTGTTTATCTTCTGCACA 1096
1566 GCAAGCCCTACGTTTACAGGGTTATCAGACACAGCCCTACCTGCTCTACAGCTTACATC 1625
1097 TTAATCGCTGTGTTTATTTACTGGGCTTCAAACTATGAAAGAAATGSCATCTAGATGGG 1156
1626 TGAACCTCATGCTCTATTACTGGGCTATCGGCTATGAGGCGCTCGGCTCCACTACTGGG 1685
1157 TGTATGATGGGAGGAAACGAGATCTCAGATGTTTATTTATTTATTTATTTATTTATTTAA 1216
1686 TTTATGATGGGAGGAAACGATTCATTCGCTGTTTACTTACTGCGGTGTGAGACCCCTCA 1745
1217 TTACCAATGCTGGCTTCCAGAACCAACAACTTTATTTGAAATTTGTTTAACTCTTGA 1276
1746 TCACCAATGCGGCTTCCCGGACCCAGGCGCTCTTTGAAATTTGTTTCCAGGCTCTAA 1805
1277 ATTTTCTTGGAGTTTGTGTTTCTCAGTTTAAATTTGATGATGATGATGATGATGATGAT 1336
1806 ACTATTTCAGGGCGCTTCTCGCTTTCTCGGTGATGATGATGATGATGATGATGATGATG 1865
1337 GAGCACTACAGCAATCAGAACTACTTCCGCGCTTCAATGATGATGATGATGATGATGATGAT 1396
1866 GGGCCGCCACCGGGAGACAGACTACTACCGAGCTGCACTGAGACACCGTGAAGTATA 1925
1397 TGAACAATTTACTCCATTTCTTAAATTTGTTGCAAAAGCGAGTTTGGATTTGATATATA 1456
1926 TGAATTTCTACAAGATCCCCAGGTCGCTGCGAGACCGGGTCAAGACCTGTTAGCAATACA 1985

Db 2577 GCCTTTTGCCTTTGGATTCTCTACTTGAACCTTGGCGTGAACCCCTCTCTCGCCTGC 2636
QY 977 ATAGGATGTTAAGTACACTTCATTTTGTGATTTAATCATCACTAGAGTCTATATGG 1036
Db 2637 CCCGTGCTGAGTACATGGCTTCTTTGAGTTTAAATACCGTCTGGAAGCCATCTCA 2696
QY 1037 ACAAGCATATATCAAGAGTTATTCGAACAACTGGATCTTGTGTTTATTTCTGCACA 1096
Db 2697 GCAGAGCTACGTTTACAGGTTATCAGACCAACCGCTACTCTGTGTATAGTTGCATC 2756
QY 1097 TTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGAAATTTGGCACTACTAGATGG 1156
Db 2757 TCAACTCTCTCTTTTACTTACTGGGCTGCGCTTCCAGGCACTCGTTCCACTCACTGG 2816
QY 1157 TGTATGATGGGAGAGAAACAGATATCTGAGATGTTATTTTGGGAGTTTCGAACTTTAA 1216
Db 2817 TTTATGACGGCTGGGGAACAGCTACATCGATGCTACTCTGGGCTGTGAATACTCTCA 2876
QY 1217 TTACATTTGGTGGCTTCCAGAACCAAACTTTTATTTGAAATTTGTTTTTCAACTTTGA 1276
Db 2877 TCACCATCGAGGACTGCCGACCCAGACGCTCTTTGAGATCGTCTCCAGCTGCTGA 2936
QY 1277 ATTTTCTTCTGGAGTTTCTGTTCTCCAGTTTAAATTTGTCAGATGAGAGATGATG 1336
Db 2937 ATTATTTTACAGGTGCTCTCGCTTTCTCTGTGATGTTGGACATGAGAGATGTTGGTG 2996
QY 1337 GAGCAGCTTACAGCCAACTCAGAACTACTTCCGCGCTGCTGATGATGACACCATTTGCCCTACA 1396
Db 2997 GGGCGCCACGGCAGGGCAGACGTTACTACCGACGCTGATGGACAGCACCGTGAAGTACA 3056
QY 1397 TGAACAATTTACTCCATTCTTAACTTTGTGCAAAAGCGAGTTCCGACTTGTATGAAATTA 1456
Db 3057 TGAACCTTCTACAAGATCCCAAGTCTGTGCAGAACCGCGTCAAGACCTGGTACGAATACA 3116
QY 1457 CATGGACTCTCAAGATGCTAGATGATCTGATTTGCTTAAAGCCCTACCACTACGG 1516
Db 3117 CTTGGCACTCAAGGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 3176
QY 1517 TCCAGTTAGCCCTCGCCATTGATGAACTTACAGCATCATCAGCAAAAGTCGACTTGTTC 1576
Db 3177 TSCGTCTGGACCTGGCCATTGACGTAACTTACAACATTTGTCAAGCAAGTGGCGCTCTCC 3236
QY 1577 AGGGTTGTGTATACACAGATGATTTATGACATGTTGCTAAGATTCAATCCGTTCTCTATT 1636
Db 3237 AGGCTTGGACCGGCAGATGATCTTCACATGCTCAAGCGACTTGGCTCAGTCTGCTACC 3296
QY 1637 TGCCTGTGACTTTGTCTGCAAAAGGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC 1696
Db 3297 TACCAATGACTATGTGTGCAAGAGGGGAGATTGGCCGAGAGATGTATATATCCAGG 3356
QY 1697 ATGAGAGTCCAAAGTTCTTGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAG 1756
Db 3357 CGGGCGAGGTGCAAGTCTGGGGGCCAGATGGAAGGCTGTCTTGGTGACACTCAAG 3416
QY 1757 CTGGCTCGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTG 1816
Db 3417 CCGGATCGGTGTTGGAGAGTAAGCTTCTGCTGTCTGGGGCGGTACAGCGGCACCG 3476
QY 1817 CCAATGTGGTGGCCCGCGGTGTCGCAATCTTTTAACTTAGACAAAGAACCTTCCAAG 1876
Db 3477 CCAATGTGGTGGCCCGCGGTTCACCAATCTCTTCACTTGGATAAGAGGACTTGAATG 3536
QY 1877 AAATTTCTAGTGCATTATCCAGATTTCTGAAAGGATCTCTATGAAGAAAGCCAG 1928
Db 3537 AGATTTTGGTGCAATACCTTCAATCTCAGAACTGCTTCCGGAAGAGGCCAG 3588

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:18:50 ; Search time 6067.19 Seconds

(without alignments)
11960.251 Million cell updates/sec

Title: US-09-855-828-3

Perfect score: 2430

Sequence: 1 atgtttaaatgcgcgacaaa.....aagaaagcctaagcaataa 2430

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estnu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_esti:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estcom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rod:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gss1:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	815.8	33.6	2056	11 AK040140	AK040140 Mus muscu
2	553	22.8	553	10 BF725470	BF725470 Bx16c03.y
3	478	19.7	527	9 AL713036	AL713036 DKZP686A
4	470	19.3	655	10 BB635459	BB635459 BB635459

C	5	430.2	17.7	437	10	BF725459
	6	402.4	16.6	881	10	BE287002
	7	363.8	15.0	1201	13	BX401127
	8	320.8	13.2	468	9	AA069559
	9	308.4	12.7	978	13	BQ688992
	10	301.4	12.4	694	9	AU137778
	11	286.8	11.8	741	13	BX104558
	12	280.8	11.6	738	12	BI736222
	13	280	11.5	423	12	BM938767
	14	279	11.5	445	14	HS3423
	15	271.2	11.2	545	10	AW465556
	16	262.2	10.8	563	12	EG304577
	17	261.6	10.6	503	9	AI150392
	18	234	9.8	247	9	AA317961
	19	232.4	9.6	270	9	AA012972
	20	224	9.2	325	10	BE982488
	21	219	9.0	696	13	BM269181
	22	216.2	8.9	518	9	AV605886
	23	216.2	8.9	747	12	BI733974
	24	212.4	8.7	215	9	AA069498
	25	211	8.7	869	14	CD327412
	26	201.6	8.3	993	13	BX370500
	27	197.2	8.1	581	9	AV605887
	28	165.6	6.8	353	9	AL120448
	29	164	6.7	376	9	AL120239
	30	162.2	6.7	674	29	CC498739
	31	137	5.6	832	12	BI827605
	32	131.2	5.4	591	29	CC571022
	33	129.8	5.3	573	12	BM354832
	34	120.6	5.0	535	9	AL928461
	35	111	4.6	920	13	BUL39545
	36	110.6	4.6	490	13	BQ639921
	37	109.2	4.5	584	12	BM882371
	38	106.8	4.4	819	13	BU287884
	39	105.6	4.3	1215	28	CC245670
	40	102.8	4.2	795	13	BU291723
	41	97.6	4.0	573	29	CG985260
	42	96.6	4.0	706	9	AJ442203
	43	94.4	3.9	800	29	CNS03HCK
	44	92.2	3.8	567	10	BF937274
	45	91.4	3.8	712	13	BX416727

ALIGNMENTS

RESULT 1
LOCUS AK040140
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:AK3069G05 product:cyclic nucleotide gated channel beta 3, full insert sequence.
ACCESSION AK040140
VERSION AK040140.1 GI:26087649
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

AK040140 2056 bp mRNA linear HTC 19-SEP-2003
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:AK3069G05 product:cyclic nucleotide gated channel beta 3, full insert sequence.

AK040140
Mus musculus (house mouse)
HTC; CAP trapper.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED 10349636

REFERENCE 2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBMED 11042159

REFERENCE AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, I., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
REFERENCE AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2056)
JOURNAL REFERENCE AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanganaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihata, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saigo, K., Saichoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
JOURNAL TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/
FEATURES	Location/Qualifiers source 1..2056 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:A430069G05" /db_xref="MGI:2404764" /db_xref="taxon:10090" /clone="A430069G05" /issue_type="thymus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate" misc_feature 1..2056 /note="cyclic nucleotide gated channel beta 3 (MGI:1352562, GB NM_013927, evidence: BLASTN, 100%, match=2055)"
ORIGIN	Query Match 33.6%; Score 815.8; DB 11; Length 2056; Best Local Similarity 77.5%; Pred. No. 2.2e-139;

Matches 1050; Conservative 0; Mismatches 252; Indels 53; Gaps 3;	
QY	1076 ACTTGTGTTTATTTCGACATTAATGCGCTGTGTTTATTACTGGGCTTCAACTATGAAG 1135
DB	2 ACTTGTGTTTTCCTGCGCATTAAGCGCTGTGTTTATTACTGGGCTTCAACTATGAAG 61
QY	1136 GAATTCGGCACTACTAGATGGGTGTATGATGGGGAAGAAACAGATATCTGAGATGTATT 1195
DB	62 GAATTCGGCTCAACTAAATGGTCTATAAAGTGAAGGACAAAGATCTGCGATGCTTTT 121
QY	1196 ATTGGGCAGTTGCACTTTAAATTAACATTGGTGGCTTCCAGAACACAAATTTATTG 1255
DB	122 ATTGGGCAGTTGCACTTTAAATTAATCTATCGGGGGCTTCCAGAGCCAGACTTCATTG 181
QY	1256 AAATTCGTTTTCACCTCTTGAATTTTTTCTGGAGTTTTTCTGTTTCTCCAGTTTAAATG 1315
DB	182 AAATTCGTTTTCACCTCTTGAATTTTTTCTGTTTCTGTTTCTCCAGCTTAAATG 241
QY	1316 GTCAGATGAGATGTGATGTGAGCAGCTPACAGCAATCAGAACTACTTCCGCGCTGCA 1375
DB	242 GTCAGATGCGTGTGATGTGAGTGGGCGAGCAACAGCCAATCAGAACTACTTCCAGCGCTGCA 301
QY	1376 TGGATGACACCACTTCCCTACATGACAAATTAATCTCCATTCCTAACTTGTGCAAAAGCAG 1435
DB	302 TGGACCATATCATTCCTACATGAAACAATCTCTATTCTCAGAGTGTGAGTATCGAG 361
QY	1436 TTGGCACTTGGTATGAATATATCATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGC 1495
DB	362 TTGGCACTTGGTGGATATATCATGGAATCACAAGAAATCCTAGATGAGTCCAATTCG 421
QY	1496 TTAAGACCTTACCACTAGCTCAGTTCAGTTAGCCCTGCCATTGATGATGAACTTACGATCA 1555
DB	422 TTGAAGAACTCCCGCAGCAATGTCAGTTGTCTATTGCCCTTGACATAAATCTCAGTATCA 481
QY	1556 TCAGCAAAAGTCAGCTTGTTCAGGGGTGTGATACACAGATGATTTATCAGATGTTGCTAA 1615
DB	482 TCAGCAAGTGGAGTTATTCAGGGCTGTGACACACAGATGTTTATGACCTGCTGCTAA 541
QY	1616 GATTGAATTCGTTCTCTATTTCGCTGTGACTTTGTGCAAAAGGAGAAATTTGCA 1675
DB	542 GATTGAATTCCTCACTATTATTATTACCTGTGACTTTGTGCAAAAGGAGAAATTTGAA 601
QY	1676 AGCAATGTATATCATCAAGCATGAGAAAGTCCAAAGTTCTTGGAGGCCCTCATGCTACTA 1735
DB	602 AAGAATGTACATCATCAACAGGAAAGTCCAAAGTCTTGGAGGCCCTCATGCTGCTC 661
QY	1736 AGTTCTGTTTACTCTGAAAGCTGGTGGTGTGTTGGAGAAATCAGCTTCTAGCAGAG 1795
DB	662 AGTTCTGTTTACTCTGAAAGCTGGTGGTGTGTTGGAGAAATTAAGCTTCTGCAAAAG 721
QY	1796 GAGGAGGAAACCGTCGAACTGCCAATGTGTCGCCACGGGTTTGGCAATCTTTTAACTC 1855
DB	722 GAGGAGGAAATCGCCGGACAGCTGATGTGTGGCCCGGATTTGCCAATCTTTTAACTC 781
QY	1856 TAGCAAAAAGACCTTCCAGAAATTTCTAGTCATTATTCAGATTTCTCAAGAGATCCTCA 1915
DB	782 TGGCAAAAAGACTCTCCAGAAATTTCTGTGCTATTATCCAACTTCTTAAAGCTCTCTCA 841
QY	1916 TGAAGAAGCCAGAGTGTCTTTTAAAGCAGAGGCTAGACCGGAGAGAACCCCTCCAA 1975
DB	842 TGAAGAAGCCAAATTTCTTTTAAAGCAGAGGGAAGACCTCTCAGGCAATCCCTGCAA 901
QY	1976 GAAAGAGTCTTGGCCCTCTCTTCCACCGAAAGAGAGACCCCAAACTGTTTAAAACTC 2035
DB	902 GACCAGGACCTGCTCTTCTTTTCCCAACAAGAGAGACACCCCGAATGCTTAAAGTTC 961
QY	2036 TCCTAGAGGACAGGAAAAGCAAGTCTTTCAGAGCTACTCAAAATTCGAAGCAGAGCAAG 2095
DB	962 TCCTAGAGAAACACAGGAAAGGTGGACCTTTGAGAGACTCTTTAAAGGAAAGAGAAAAACA 1021
QY	2096 CAGCTCAGAGAAAGAAAAATTCCTGAAGGAGAGAGGAAAGGAAAGAAAAATCAAGATA 2155
DB	1022 CCACTCAGAA-----ATTAAGGTTGAAA 1043

ORIGIN

QY 2156 AACAAAGAAATGAAGATAAACAAGAAAGAAATCAAGATAAAGAAAGAAAGAAATGAAG 2215
 Db 1044 GTTCCAAAGAAAGAAAGAAAGAAAGAAATATGAAGACAAAGAAAGAAAGAAAGTACGAG 1103
 QY 2216 ATAAAGATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2275
 Db 1104 AAAAAGAAGA-----AAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1149
 QY 2276 GTCCATTTCAGTGGAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2335
 Db 1150 GTTCTATTACAGTGGAGGAAGAAAGTCCCAATCAATTAATAGGAGTTCCTCCCAAGAGC 1209
 QY 2336 CTTCTCGTCAATCACTCATATCAGCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2395
 Db 1210 ATGCTTATCAATGATCATCAGCAACATGG-TCCTGCTACTGAGAGTGGAGGAAGAGATT 1268
 QY 2396 TTACTATTGAAGTCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2430
 Db 1269 TGACTATCAAGTCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1303

RESULT 2
 BF725470
 LOCUS
 DEFINITION
 bxl6c03.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bxl6c03 5', mRNA sequence.
 BF725470
 BF725470.1 GI:12041381
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 553)
 Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
 NEIBANK: EST analysis and bioinformatics for ocular genomics
 Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
 Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 16 row: C column: 03
 Seq primer: M13RPL reverse primer (ABI).
 Location/Qualifiers
 1..553
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="bxl6c03"
 /tissue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Human Iris cDNA (Un-normalized, unamplified): BX"
 Note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTCTTACATCGGAGCGCGGCC(T)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
 FEATURES
 source

RESULT 3
 AL713036
 LOCUS
 DEFINITION
 DKFZp686A1695_r1 686 (synonym: h1ccc3) Homo sapiens cDNA clone DKFZp686A1695 5', mRNA sequence.
 AL713036
 AL713036.1 GI:19696392
 EST.
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 527)
 Bloecker,H., Boecker,M., Brandt,P., Mewes,W., Weil,B. and Wiemann,S.
 EST (Bloecker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann,S.)
 Unpublished (1999)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GfB (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the

Query Match 22.8%; Score 553; DB 10; Length 553;
 Best Local Similarity 100.0%; Pred. No. 3.8e-91;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 GTTTATTCTCACAATTAATGCCTGTGTTTATTACTTGGGCTTCAAACTATGAAGAAATGG 1142
 Db 1 GTTTATTCTGCACANTTAATGCCTGTGTTTATTACTTGGGCTTCAAACTATGAAGAAATGG 60
 QY 1143 CACTACTAGATGGGTGATGATGGGAAAGAAAGAGATCTGAGATGTTATTATTGGGC 1202
 Db 61 CACTACTAGATGGGTGATGATGGGAAAGAAAGAGATCTGAGATGTTATTATTGGGC 120
 QY 1203 AGTTGGAACCTTATTACCATTGGTGGCTTCCAGAACCAACAACCTTTATTGAAATGT 1262
 Db 121 AGTTGGAACCTTATTACCATTGGTGGCTTCCAGAACCAACAACCTTTATTGAAATGT 180
 QY 1263 TTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTCTTCCAGTTAAATTTGTCAGAT 1322
 Db 181 TTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTCTTCCAGTTAAATTTGTCAGAT 240
 QY 1323 GAGAGATGTTGATTCGAGCAGCTCAGCCATCAGAACTACTTCCGCGCTGCATGGATGA 1382
 Db 241 GAGAGATGTTGATTCGAGCAGCTCAGCCATCAGAACTACTTCCGCGCTGCATGGATGA 300
 QY 1383 CACCAATGCCCTACATGAACAAATTAATCTCATTCTTAACTTGTGCAAAAGCGAGTTCGGAC 1442
 Db 301 CACCAATGCCCTACATGAACAAATTAATCTCATTCTTAACTTGTGCAAAAGCGAGTTCGGAC 360
 QY 1443 TTGTTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAGAC 1502
 Db 361 TTGTTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAGAC 420
 QY 1503 CCTACCAACTAGGTCAGTTAGCCCTGCGCAATGATGTAACCTCAGCATCATCAGCAA 1562
 Db 421 CCTACCAACTAGGTCAGTTAGCCCTGCGCAATGATGTAACCTCAGCATCATCAGCAA 480
 QY 1563 AGTCGACTTGTTCAGGGCTTGTGATACACAGATGATTATCAGATGTTGCTTAAGATTGAA 1622
 Db 481 AGTCGACTTGTTCAGGGCTTGTGATACACAGATGATTATCAGATGTTGCTTAAGATTGAA 540
 QY 1623 ATCCGTTCTCTAT 1635
 Db 541 ATCCGTTCTCTAT 553

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arahawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp/
URL: <http://genome.gsc.riken.go.jp/>
Carrinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1611-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

genes. *Genome Res.* 10 (10), 1679-1690 (2000).
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsumi,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.,
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,Y., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

```

tissues.
Location/Qualifiers
1. .635
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A430069G05"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate
thymus"

```

/note="Site 1: Salt; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTCVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adaptor of sequence [5'-GAGAGAGAGATCTCGATTAATTAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN
 Query Match 19.3%; Score 470; DB 10; Length 655;
 Best Local Similarity 84.2%; Pred. N.5e-76;
 Matches 553; Conservative 0; Mismatches 101; Indels 3; Gaps 2;
 QY 1078 TTGCTGTTATTCTGCACATTAAATGCTCTGTTTATTATTCGGGTTCAAACTATGAAGGA 1137
 FLC 1.1%

contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5',
 GAGAGAGAGAGATCCAGAGACTCTTTTITTTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5', GAGAGAGAGATCTCGATTAAATAATATCCCTCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(-) after bulk excision from Lambda
 FLC I."

ORIGIN

Query Match 19.3%; Score 470; DB 10; Length 655;
 Best Local Similarity 84.2%; Pred. No.5e-76;
 Matches 553; Conservative 0; Mismatches 101; Indels 3; Gaps 2;

1078 TTGCTGTTTATCTGCACATTAAATGCTGTGTTTATTACTGGGTTTCAAACTATGAAGGA 1137

```
Db 1 TTGCTGTTCTCTGCTGACATTAACCCCTGTGTTTATTACTGGGCTTCAGACTATGAAGA 60
QY 1138 ATTGGCACTACTAGATGGGTGATGATGGGGAAGAAACAGTATCTGAGATGTTATTAT 1197
Db 61 ATTGGCTCAACTAATGGGTCTATATGTTGGTGAAGCAACAAGTATCTGGAATGCTTTAT 120
QY 1198 TGGGCAAGTTCGAACCTTAATTAACCATTTGTTGGCTTCGAGAACCAACAACCTTTATGAA 1257
Db 121 TGGGCAAGTTCGAACCTTTAATTAATTAATTCGAGGAGCTTCGAGAGCCACAGACTTCATTGAA 180
QY 1258 ATGTTTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTCTCCAGITTAATTTGGT 1317
Db 181 ATGTTTTTCAACTCTTGAATTTTTTCTGGGTTTTTGTCTCCAGCTTAATTTGGT 240
QY 1318 CAGATGAGAGATGTTGATTCGAGCAGCTACAGCAATTCAGAACTACTTCCGCGCTTCGATG 1377
Db 241 CAGATCGGTGATGTTGATTCGGGCGAGCAACAGCAATTCAGAACTACTTCCAGCGCTGCATG 300
QY 1378 GATGACACCAATTCCTACATGACATTAATTAATTAATTAATTAATTAATTAATTAATTA 1437
Db 301 GACCATATCATTCCTGACATGAACAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
QY 1438 CGGACTTGTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1497
Db 361 CGGACTTGTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY 1498 AGACCCCTACCAACTAGCTGAGTTAGCCCTGCGCAATTCAGTGAATTCAGCATCATC 1557
Db 421 GAGAACCTCCCGACAGCAATTCAGTGTGTTATTTGCGCTTGACATAAATTCAGTATCATC 480
QY 1558 AGCAAAAGTCGACTGTTTCAAGGTTTGTGATACACAGATGATTTATGACATGTTGCTAAGA 1617
Db 481 GACAAGTGGAGTATTCAGGCTGTGACACACAGATGATTTATGACCTGCTGCTAAGA 540
QY 1618 TTGAATTCCTGTTCTTATTTGCTGAGTCTTTGCTGCAAAAGGAGAAATTCGCAAG 1677
Db 541 TTGAATTCCTGTTTATTTATTTACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
QY 1678 GAATGTTATCATCAGCATGAGATGCAAGTTCCTGAGGCTGATGTTGTTGTTGTTGTTGTT 1734
Db 601 --AATGTACATCATCAA-CAGGAGAGTCCAAAGTCTCTTGGAGGCTGATGTTGTTGTTGTT 654
```

```
RESULT 5
BF725469/c 437 bp mRNA linear EST 05-JAN-2001
LOCUS bx16c03.x1 Human Iris cDNA (Un-normalized, unamplified): BX Homo
DEFINITION sapiens cDNA clone bx16c03 3', mRNA sequence.
ACCESSION BF725469
VERSION BF725469.1 GI:12041380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 437)
Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 16 row: c column: 03
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. 437
/mol_type="mRNA"
```

```
/db xref="taxon:9606"
/clone="bx16c03"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Iris cDNA (Un-normalized, unamplified):
BX"
/notes="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the Superscript Plasmid System
full details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTAGTTCATGATCGAGCGCGCC(T)15-3']. Not I/blunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (NISC)."
```

ORIGIN

```
Query Match 17.7%; Score 430.2; DB 10; Length 437;
Best Local Similarity 99.3%; Pred. No. 1.2e-68;
Matches 432; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1759 GGGTCGGTGTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTGCC 1818
Db 437 GGGTCGGTGTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTGCC 378
QY 1819 AATGTGTGGCCCGCGGTTTGGCAATCTTTAACTCTAGACAAAGACCCCTCAAGAA 1878
Db 377 AATGTGTGGCCCGCGGTTTGGCAATCTTTAACTCTAGACAAAGACCCCTCAAGAA 318
QY 1879 ATTCTAGTGCATTTATCCAGATTCCTGAAAGATTCCTCATGAAGAAGCCAGAGTGCTTTA 1938
Db 317 ATTCTAGTGCATTTATCCAGATTCCTGAAAGATTCCTCATGAAGAAGCCAGAGTGCTTTA 258
QY 1939 AAGCAGAAAGGCTAAGACCGCAGAAAGCAACCCCTCAAGAAAGATCTTGGCCTCTCTTC 1998
Db 257 AAGCAGAAAGGCTAAGACCGCAGAAAGCAACCCCTCAAGAAAGATCTTGGCCTCTCTTC 198
QY 1999 CCACGAAAGAGAGACACCCAACTGTTTAAACTCTCTAGGAGGACAGGAAAGCA 2058
Db 197 CCACGAAAGAGAGACACCCAACTGTTTAAACTCTCTAGGAGGACAGGAAAGCA 138
QY 2059 AGTCTTGAAGACTACTCAAAATTGAAGCGAGAGCAAGCAGCTCAGAGAAAGAAATTTCT 2118
Db 137 AGTCTTGAAGACTACTCAAAATTGAAGCGAGCAGCAGCTCAGAGAAAGAAATTTCT 78
QY 2119 GAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2178
Db 77 GAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 18
QY 2179 CAAAAGAGAAATGAA 2193
Db 17 CAAAAGAGAAATGAA 3
```

RESULT 6

```
BE287002 881 bp mRNA linear EST 26-OCT-2000
LOCUS 601097229F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3496015 5',
DEFINITION tRNA sequence.
ACCESSION BE287002
VERSION BE287002.1 GI:9165707
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

REFERENCE 1 (bases 1 to 881)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM8547 row: i column: 08
 High quality sequence stop: 774.
 Location/Qualifiers
 1. 881
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:3496015"
 /tissue type="tumor, gross tissue"
 /dev stage="7 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Mam5"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

ORIGIN

Query Match 16.6%; Score 402.4; DB 10; Length 881;
 Best Local Similarity 73.9%; Pred. No. 1.2e-63;
 Matches 548; Conservative 0; Mismatches 171; Indels 23; Gaps 2;

QY 1459 TGGGACTCTCAAGAATGCTAGATGAGTGTGATTTGCTTAAGACCCCTACCACTAGGTC 1518
 Db 1 TGGAACTCACAAAGAAATCTAGATGATGCTCCACTTGTGAGAACCTCCCGACAGCATG 60

QY 1519 CAGTTAGCCCTGCGCATGTGATGTGAATTCAGCATCATCAGCAAGTCGACTTGTTCAG 1578
 Db 61 CAGTTGTCTATTGCGCTTGACATAAATCTCAGTATCATCGACAAGTGGAGTTATTCAAG 120

QY 1579 GGTGTGTATACAGAGATGATTATGACATGTTGCTAGATTGAAATCCGTTCTATTTC 1638
 Db 121 GCGTGTGACACAGATGATTATGACCTGCTGCTAAGATGAAATCCACTATTATTTA 180

QY 1639 CTGTGTGACTTTGTCTCAAAAGGGAGAAATTTGGCAAGAAATGTATATCATCAAGCAT 1698
 Db 181 CTGTGTGACTTTGTCTCAAAAGGGAGAAATTTGGAAAGAAATGTATATCATCAACAC 240

QY 1699 GGAGAAGTCCAAAGTCTTGGAGGCCCTGTGTTACTTAAAGTCTTGGTTACTCTGAAAGCT 1758
 Db 241 GGAGAAGTCCAAAGTCTTGGAGGCCCTGTGTTACTTAAAGTCTTGGTTACTCTGAAAGCT 300

QY 1759 GGGTCGGTGTGTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTGAACCTGCC 1818
 Db 301 G-----GCTTCTGCAAAAGGAGGAGGAATGCGGACAGCT 339

QY 1819 AATGTGTGGCCCGCCGCGTTTGCATTTTAACTCTAGACAAAAGCCCTCCCAAGAA 1878
 Db 340 GATGTGTGGCCCGCCGCGTTTGCATTTTAACTCTAGACAAAAGCTCTCCCAAGAA 399

QY 1879 ATTCTAGTCAATATCCAGATTTCTGAAGGATCTCTCATGAAGAAACCCAGAGTCTTTTA 1938
 Db 400 ATTCTAGTCAATATCCAACTTTCTAAAGCTCTCTCATGAAGAAACCCAAATCTTTTA 459

QY 1939 AAGCAGAGCTTAAGCCGAGAGCAACCCCTCCCAAGAAAGATCTTCCCTCTCTTC 1998
 Db 460 AGCCAGAGGAGGAGACCACTCAGGCAATCCCTGCAAGACCCAGGACCTGCTTCTTTTC 519

QY 1999 CCACCCAAAGAGAGACACCCAAACTGTTTAAACTCTCTCTAGGAGGACAGGAAAGCA 2058
 Db 520 CCACCCAAAGAGAGACACCCCGAATGCTTAAAGTTCTCTCTAGGACACACAGAGGTTGG 579

QY 2059 AGTCTTGCAGACTACTCTAAATTTGAAGCGAGAGCAAGCAGCTCAG--AAGAAAGAAAT 2116
 Db 580 ACCTTGAAGACTCTCTTAAGGAAAGAGAAAAACAACCACTCAGAAATTAACCGTGAA 639

QY 2117 CTGAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2176
 Db 640 GTTCCACAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699

QY 2177 AACAAAGAGAAATGAAGATAA 2198
 Db 700 AGCAGAAAGAGAAAGAAAGAA 721

RESULT 7
 EX401127
 LOCUS
 DEFINITION BX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 cDNA clone CSODK009YE13 5-PRIME, mRNA sequence.
 ACCESSION BX401127
 VERSION BX401127.1 GI:30614460
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7817.r For
 more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODK009AC07QPI&cluster=7817.r>. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODK009AC07QPI.
 Location/Qualifiers
 1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK009YE13"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source

ORIGIN

Query Match 15.0%; Score 363.8; DB 13; Length 1201;
 Best Local Similarity 60.8%; Pred. No. 1.2e-56;
 Matches 611; Conservative 35; Mismatches 353; Indels 6; Gaps 5;

QY 861 AAATGAGCTAGGAAACACACACGACTCTACAAATTTCAAAATTTCAATTCGATCGCATCAAT 920
 Db 8 AAAGGATATGGAATTAATCACTACCTGAAAGTCTCGCGGCTTCAAGATGAGCACTGTCAGCCT 67

QY 921 AATACCAATTTGATATTTGCTACCTCTTTCTTTGGGTTTAAATCCAAATGTTTGAAGCAATAG 980
 Db 68 CCGTCCCTTGGATTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCTCGCGTGCWCCG 127

QY 981 GATGTTAA--GTACACTTCATTTTGAATTTAATCATCACCTAGATGCTATAATGGAC 1038

Db	128	CTGTTAAATGATCATGCGCTCTTCGAGTTTAAACAGCGCGTGAATCCATCTCAGC	187
QY	1039	AAAGCATATATCTACAGAGTTATTCGAACAATGAGTATCTGCTGTTTATTCTGCACAT	1098
Db	188	AAAGCTACGTGTACAGGTCATCAGGAYCAGAYTACCTCTTACAGCCTGCATTG	247
QY	1099	ATGCTCTGTTTATTTACTTGGCTTCAAACTATGAAGAAATGGCACTACTAGATGGTG	1158
Db	248	AATTCCTGCTTTTATTTACTTGGCATCGGCTATCAGGGCTCGGCTCCACTCACTGGGT	307
QY	1159	TATGATGGGGAAGAAACAGATATCTGAGATGTTATTATGGCAGTTCGAATTTAAT	1218
Db	308	TACATGCGCTGGGAAACAGTTATATTCGCTGTACTTCTGCTGTGAACMCTCATC	367
QY	1219	ACCATTTGGTGGCTTCCAGAACCAAACTTATTTGAAATGTTTTCCTCACTCTGAA	1278
Db	368	AVCATCGGGGGCTGCTGACCCCAAGAVACTTTTGAATTTGCTTCCAGCTGTGAA	427
QY	1279	TTTTTCTGAGTTTTTGTGTTCTCCAGTTTAAATTTGTCAGATGAGATGTATTGA	1338
Db	428	TATTTCAAGGGCTGCTTTGCTTCTGTGATGATTTGGACAGATGAKAGATGTGTAGG	487
QY	1339	GCAGCTACAGCCCAATCAGAACTACTTCCGGCGCTGCATGATGACACCACTTGCATG	1398
Db	488	GCCGCCACCG-CAGACAGACCTACTACCGCAGCTGCATGCACAGCAGGTGAATAC	546
QY	1399	ACAATTTACTCCATTCCTAACTTTGTCAAACGAGTTCCGACTTTGGTATGATATACA	1458
Db	547	AATTTTACAAAGATCCCAAGTCCGTGCAGAACGAGTCAAGACCTGGTAAAGATCAC	606
QY	1459	TGGGACTCTCAAGAATGTAGATGAGTCTGATTTGCTTAAGACCTCAACACTACGGTC	1518
Db	607	TGGCACTCGCAAGCATCTGATGATGATGAGCTGATGCTGCAGCTTCCAGACAAGATG	666
QY	1519	CAGTTAGCCCTCGCATTTGATGAACTTCAGATCATCAGCAAGAGTGTGCTTCAAG	1578
Db	667	CGGCTGAGCTCGCATCGCATGAACTACAACATCGTTAGCAAGTGCAGCTCTTTCAG	726
QY	1579	GGTTGTGATACAGAGATTTATGACATGTCGATGATTTGAATTCGGTCTCTATTG	1638
Db	727	GGCTGTACCGCGCAGATGATCTTTGATGATGATGAGAGGCTTCGCTGTGTCTACCTG	786
QY	1639	CCTGGTGAATTTGCTGCAA-AAAGGAGAAATTTGCAAGAAATGATATCATCAAGCA	1697
Db	787	CCCAACGACTATGTGTCAAGAAVGGSSAGATCGGCGGTGAGATGTACATCATCCAGG	846
QY	1698	TGGAGAGTCAAGTCTTGGAGCCCTGATGTTAAAGTTCTGTTACTCTGAAAGC	1757
Db	847	AGGCAAGTGCAGGCTTGGGCGSCCTGTATGGGAAATCTGTCTGTGA-GCTKCAASY	905
QY	1758	TGGCTCGTGTTCGGAATATCAGCTTCTAGCAGCAGGAGGAGAAACCGTCAACTGC	1817
Db	906	KSSATYGTGTTTGSAGMAWAAGCTTCTGCTGTTTGGGGCGGCAA-DGGCGCAGGCC	964
QY	1818	CAATGTGGTCCCAAGGTTTTCGAATCTTTTAACTCTTACAA 1862	
Db	965	CAAAAGTSGSSSGSGSTTACVAMCTCTTATCTTATCTTATGSAATAAA 1009	
RESULT 8			
AA069559			
LOCUS			
DEFINITION			
zf75a04.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone			
IMAGE:382734 5', mRNA sequence.			
ACCESSION			
AA069559			
VERSION			
AA069559.1 GI:1576971			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 468)			

AUTHORS
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Pavello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Frange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

TITLE
Generation and analysis of 280,000 human expressed sequence tags

JOURNAL
Genome Res. 6 (9), 807-828 (1996)

MEDLINE
97044478

PUBMED
8889549

COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: es@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 874 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 382.

FEATURES
Location/Qualifiers
source
1...468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1290991"
/db_xref="taxon:9606"
/clone="IMAGE:382734"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/note="Organ: pineal gland; Vector: p7T3D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN		Query Match	13.2%;	Score 320.8;	DB 9;	Length 468;
		Best Local Similarity	97.9%;	Pred. No. 1.2e-48;		
		Matches 325;	Conservative	0;	Mismatches 7;	Indels 0; Gaps 0;
QY	19	AAAGTCAACAAGGTGAAGCCTATAGGAGAGAACAAATGAGAAATGAACAAAGTTCTCGTCGG	78			
Db	2	AAAGTCAACAAGGTGAAGCCTATAGGAGAGAACAAATGAGAAATGAACAAAGTTCTCGTCGG	61			
QY	79	AATGAAGAAGGCTCTCACCAGTAATCAGTCTCAGCAAAACACAGCAGGAAGAAAC	138			
Db	62	AATGAAGAAGGCTCTCACCAGTAATCAGTCTCAGCAAAACACAGCAGGAAGAAAC	121			
QY	139	AAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACTCTGAGAGCCACAC	198			
Db	122	AAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACTCTGAGAGCCACAC	181			
QY	199	ACCAACATACAGACAAACTCTCCAGAAAAATTCCTCTGGAGATCTGACCAACACCT	258			
Db	182	ACCAACATACAGACAAACTCTCCAGAAAAATTCCTCTGGAGATCTGACCAACACCT	241			
QY	259	GACCTCAAAATGCAGCAGAACCAACTGGAAACAGTGCAGAGCAGAGAAATGGACCCC	318			
Db	242	GACCTCAAAATGCAGCAGAACCAACTGGAAACAGTGCAGAGCAGAGAAATGGACCCC	301			
QY	319	GGGAAAGAGGTCCTCAAAACAGCCCAACAAACAA	350			
Db	302	GGGAAAGAGGTCCTCAAAACAGTTCACCCCTAGAA	333			

RESULT 9
BQ068992

```

LOCUS      BQ068992              978 bp      mRNA      linear      EST 02-APR-2002
DEFINITION AGENCOURT_6740166 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802872
            5', mRNA sequence.
ACCESSION  BQ068992
VERSION    BQ068992.1 GI:19898038
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 978)
            NIH-MGC http://mgi.nci.nih.gov/
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabs-rc@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCW2037 row: p column: 09
            High quality sequence stop: 726.
FEATURES   Location/Qualifiers
            source
            1..978
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5802872"
            /tissue_type="neuroblastoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_47"
            /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; CDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
ORIGIN
Query Match      12.7%; Score 308.4; DB 13; Length 978;
Best Local Similarity 67.7%; Pred. No. 1.8e-46;
Matches 432; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

Qy 1326 AGATGTGATTGGAGCAGCTACAGCCATCAGAACTACTTCGGGCGCTGCATGGATGACAC 1385
Db 1 AGATGTGTAGGGGCCGCCAGCGGGGACAGACCTACTACCGAGCTGCATGGACGAC 60

Qy 1386 CATTCGCTACATGAACAATTACTCCATTCCTAACTGTGTCAAAGGAGTTCGGACTTG 1445
Db 61 GGTGAAGTACATGAATTTCTACAGATATCCCAAGTCCGTCGACAGCGGCTCAAGACCTG 120

Qy 1446 GTATGAATATACATGGGACTCTCAAGAATGCTAGATGAGTCTGATTGCTTAAGACCCT 1505
Db 121 GTACGAGTACACCTGGCACTCGAAGCATGCTGGATGAGTCAAGCTGATGTCGAGCT 180

Qy 1506 ACCAACTACGGTCCAGTAGCCCTTCGCCATGATGAACTTCAGCATCATCAGCAAGT 1565
Db 181 TCCAGACAAGATGGCGTGGACCTTCGCATCGACGTGAATCAACATCGTTAGCAAGT 240

Qy 1566 CGACTTCCTCAAGGGTGTGATACACAGATGATTTATGACATGCTGCTAAGATTGAATC 1625
Db 241 CGACTCTTCAGGGCTGTGACCGGAGATGATCTTGACATGCTGAAGAGGCTTCGCTC 300

Qy 1626 CGTTCCTATTGCTGGTCACTTTGCTGCAGAAAGGAGAAATTTGGCAAGAAATGTA 1685
Db 301 TGTGTCTACTGCTCCCAACACTATGTGTGCAAGAGGGGGAGATCGGCGGTGAGATGTA 360

```

```

Qy 1686 TATCATCAAGCATGGAGAAATCCAACTTCTTGAGGCCCTGATGGTACTAAAGTTCTGGT 1745
Db 361 CATCATCCAGGAGGCAAGTGCAGTCTTGGGCGCCCTGATGGAAATCTGTGCTGGT 420

Qy 1746 TACTCTGAAAGCTGGGTGCGTGTTCGAGAAATTCAGCCCTTCAGCAGAGGAGGAAA 1805
Db 421 GACGCTGAAAGCTGGATCTGTGTTTGGAGAAATAAGCTTGTGCTGTTGGGGGGGAAA 480

Qy 1806 CCGTCGAACTGCCAAATGTGTGCGCCACCGGTTTCCTCAATCTTTAACTCTAGACAAA 1865
Db 481 CCGCGCACGCGCAACGTGTGCGGCGCGGGTTTACCAACCTCTTCATCCTCGATAAGAA 540

Qy 1866 GACCTCCAGAAATTTCTAGTCATTCAGATTCGAAAGATCCTCATCAAGAAAGC 1925
Db 541 GGACCTGAATGAGATTTTGGTGCATTTATCCTGAGTCTCAGAGTTACTCCGGAAGAAAGC 600

Qy 1926 CAGAGTGTCTTTTAAGCAGAGGCTTAAGACCCAGAAG 1963
Db 601 CAGGCGCATGCTGAGAAAGCAACAATAGCCCAAGGAGG 638

RESULT 10
LOCUS     AU137778              694 bp      mRNA      linear      EST 02-AUG-2002
DEFINITION AU137778 PLACE1 Homo sapiens cDNA clone PLACE1007225 5', mRNA
            sequence.
ACCESSION  AU137778
VERSION    AU137778.1 GI:10999299
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 694)
            Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
            HRI human cDNA project
            Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES   Location/Qualifiers
            source
            1..694
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="PLACE1007225"
            /tissue_type="placenta"
            /clone_lib="PLAC1"
            /note="Vector: pME18SFL3"
ORIGIN
Query Match      12.4%; Score 301.4; DB 9; Length 694;
Best Local Similarity 66.3%; Pred. No. 3.8e-45;
Matches 445; Conservative 0; Mismatches 225; Indels 1; Gaps 1;

Qy 1049 TCTACAGAGTTATTCGACAACTGATGATCTGCTGTTTATTCACATTAATCCCTGTG 1108
Db 20 TCTGAGGGTTCATCAGGACCAAGCCCTTCTCTACAGCTCATTTGAATTCCTGTC 79

Qy 1109 TTTATTACTGGGCTTCAAACTATGAAGAAATGGCACTACTAGATGGGTGTATGATGGG 1168
Db 80 TTTATTACTGGGATCGGCTATCAGGCGCTCCGCTCCACTCACTGGGTTTACGATGGC 139

```

QY	1169	AAGGAAACGAGTATCTGAGATGTTATTTATTGGCGAGTTCGAACTTTAAATTACCAATGGTG	1228
Db	140	TGGGAAACAGTTTATTTTCGCTGTTACTTTTCTGTGAAGACCCATCAACCATCGGG	199
QY	1229	GCCTTCGAGAACCAAACTTTATTTGAAATGTTTTTCAACTCTTGAATTTTTTTCTG	1288
Db	200	GGCTGCTGACCCCAAGACACTCTTTTGAATTTGTCTTCCAGCTGCTGAAATTTATTTCACGG	259
QY	1289	GAGTTTGTGTCTCTCCAGTTTAAATTCGTGAGATGTGATTGGAGCAGCTACAG	1348
Db	260	CGGTCCTTTGCTTCTCTGTGATGATCGACAGATGAGAGATGTGGTAGGGCGCCACCG	319
QY	1349	CCAAATCAGAACTACTTCCGGCCCTGCATGATGATGACACCAATGCGCTCATGAACAATTACT	1408
Db	320	CGGGACAGACCTACTACCGCAGCTGCATGGACAGACCGGTGAAGTACATGAAATTTCTACA	379
QY	1409	CCATTCTTAACTTGTGCGAAAGCGAGTTCCGACTTCGGTATGATATACATATGGCACTCTC	1468
Db	380	AGATCCCCCAAGTCCGTGCGAAGCCGCGTCAAGACCTGGTACGATACACCTGGCACTCGC	439
QY	1469	AAAGAATGCTAGATGAGTCTCATTTGCTTTAAGACCCCTACCAACTACCGTCCAGTTAGCCC	1528
Db	440	AAGCATGCTGATGAGTACAGACTGATGGTGCAGCTTCCAGACAAGATGCGGCTGGACC	499
QY	1529	TCGCCATTGATGTGAACTTTCAGATCATCAGCAAAAGTCGACTTGTTCAGAGGTTGTGATA	1588
Db	500	TCGCCATCGACGTGAACCTACCAACATCGTTAGCAAAGTCGCACTCTTTCCGGGCTGTGACC	559
QY	1589	CACAGATGATTTATGACATGTTGCTTAAGATTGAAATCGTTCTCTATTTCGCTGGTGACT	1648
Db	560	GGCAGATGATCTTTGACATGCTGAANAGGCTTCGCTCTGTTGTCTACTCTGCCCAACGACT	619
QY	1649	TTGTCTGCAAA-AAGGGGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGAGAGATC	1707
Db	620	ATGTGTGCAAGAGGGGGAAATCGGCGTGAGATGTATCATCATCCANGCAAGGCAAGTG	679
QY	1708	CAAGTTCTTGG	1718
Db	680	CAAGGTCNTGG	690

RESULT 11
 BX104558
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

741 bp mRNA linear EST 06-FEB-2003
 BX104558 Soares pineal gland 3NDHPG Homo sapiens cDNA clone
 IMAGE:5998P13890 ; IMAGE:384252, mRNA sequence.
 BX104558
 BX104558.1 GI:27832995
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 741)
 Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
 Radelof,U., Schneider,D. and Korn,B.
 Human Unigeneset - RZPD3
 Unpublished (2003)
 Contact: Ina Rolfes
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE5998P13890.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
[http://www.rzpd.pl/cgi/cloneCards/cgi-](http://www.rzpd.pl/cgi/cloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972)
[bin/showLib.pl.cgi?response?libNo=972](http://www.rzpd.pl/cgi/cloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972) Contact: Ina Rolfes
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information Seq primer:

```

M13r, Primer sequence: TTTCCACACAGGAACACAGCTATGAC.
Location/Qualifiers
1. .741
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TMAG998P13890 ; IMAGE:384252"
/tissue_type="brain, pineal gland"
/dev_stage="adults (ages 18, 20, 48)"
/lab_host="DH10B"
/clone_lib="Soares pineal gland 3NbHPG"
/notes="1st strand cDNA (prepared from post mortem tissue)
was primed with a Not I - Oligo(dT) primer [5].
TTTCCACATCAAGTGGAGCGCGCGTATTTTATTTT 3' ],
double-stranded cDNA was ligated to EcoRI adaptors
5'-AATCGCGACAGG-3' and 5'-CTCGTGGCG-3' (Pharmacia),
digested with NotI and cloned into the NotI and EcoRI
sites of the pTR73D-PacI vector. Library went through one
round of normalization, to Cot38. Library constructed by
Berto Soares and M. Fatima Bonaldo"

```

ORIGIN

Query Match	11.88;	Score 286.8;	DB 13;	Length 741;
Best Local Similarity	97.7%;	Pred. No. 1.8e-42;		
Matches 291;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	53	ATGAGAATGAACAAAGTTCTCGTCCGGAATGAAGAAGGCTTTCACCCAAAGTAATCAGTCTC	112	
Db	1	ATGAGATGAACAAAGTTCTCGTCCGGAATGAAGAAGGCTTTCACCCAAAGTAATCAGTCTC	60	
Qy	113	AGCAAAACACAGCACAGCAAGGAGAAACAAAGGTGAGAGAAATCTCTCAAAACCAAGTCAA	172	
Db	61	AGCAAAACACAGCACAGCAAGGAGAAACAAAGGTGAGAGAAATCTCTCAAAACCAAGTCAA	120	
Qy	173	CTCCAGTCACTCTGGAAGAGCCACACACCACATACAAAGCAAAACTCTCCAAGAAAAATT	232	
Db	121	CTCCAGTCACTCTGGAAGAGCCACACACCACATACAAAGCAAAACTCTCCAAGAAAAATT	180	
Qy	233	CCTCTGGAGATCTGACACAAACCTGACCCCTCAAAATGCGAGCAGAACCACTGGAAACAG	292	
Db	181	CCTCTGGAGATCTGACACAAACCTGACCCCTCAAAATGCGAGCAGAACCACTGGAAACAG	240	
Qy	293	TGCCAGAGCAGAAGGAATGACCCCGGGAAGAAGGTCCCAAAACAGCCCAACAAAACAA	350	
Db	241	TCCAGATCTGACAGGATGATCTCCCGGGAAGAAGGTCCCAACAGTTGACCCCTAGAA	298	

RESULT 12	REFERENCE
BI736222	AUTHORS
LOCUS	TITLE
DEFINITION	JOURNAL
ACCESSION	COMMENT
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

BI736222 738 bp mRNA linear EST 20-SEP-2001
 603359912f1 NTH_MGC_94 Mus musculus cDNA clone IMAGE:5367194 5',
 mRNA sequence.
 BI736222
 BI736222.1 GI:15713235
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 738)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: J1AM11934 row: 9 column: 03


```

QY 1458 ATGGAGCTCTCAAGAATGCTAGATGAGTGTGATTTGCTTTAAGACCTTACCACCTACGGT 1517
    |||||
Db 229 ATGGAAGTCTCAAGAATGCTAGATGAGTGTGATTTGCTTTAAGACCTTACCACCTACGGT 170
    |||||
QY 1518 CCAGTTAGCCTCCGATTCATGCTGACTTCACATCATCAGCAAGTGCAGTGTGTTCAA 1577
    |||||
Db 169 GCAGTTGCTGATTCGCTTCACATAAATTCAGTATCATCGCAAGTGGAGTTATTCAA 110
    |||||
QY 1578 GGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATT 1637
    |||||
Db 109 GGGCTGTGACACAGATGATTTATGACCTGCTGCTAAGATTGAAATCCACTATTATT 50
    |||||
QY 1638 GCCTGTGACTTTGTCTGCAAAAGGGAGAAA 1669
    |||||
Db 49 ACCTGTGTGACTTTGTCTGCAAAAGGGAGAAA 18
    |||||

RESULT 14
H53423 H53423 445 bp mRNA linear EST 20-SEP-1995
LOCUS yf86a09.r1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone
DEFINITION IMAGE:231160 5', mRNA sequence.
ACCESSION H53423
VERSION H53423.1 GI:993570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissee,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.,
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
MEDLINE 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
PUBMED Tel: 314 286 1800
COMMENT Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 903
High quality sequence stops: 302
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 903 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 302.
Location/Qualifiers
1..445
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3861151"
/db_xref="taxon:9606"
/clone="IMAGE:231160"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares pineal_gland_N3HPG"
/clone="organ: pineal gland; Vector: pT773D (Pharmacia)
with a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGGTTTATTTTATTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT773
vector (Pharmacia). Library constructed by Bento Soares
and M.Patina Bonaldo."

```

ORIGIN

```

Query Match 11.5%; Score 279; DB 14; Length 445;
Best Local Similarity 90.1%; Pred. No. 5.4e-41;
Matches 311; Conservative 0; Mismatches 27; Indels 7; Gaps 1;

QY 1 ATGTTTAAATCGCTGACAAAGTCAACAGGTGAAGCCTATAGGAGAGAACAAATGAGAAAT 60
    |||||
Db 39 ATGTTTAAATCGCTGACAAAGTCAACAGGTGAAGCCTATAGGAGAGAACAAATGAGAAAT 98
    |||||
QY 61 GAACAAAGTTCTCGTCGGAATGAAGAAGGCTCTCAACCAAGTAAATCACTCTCAGCAAAACC 120
    |||||
Db 99 GAACAAAGTTCTCGTCGGAATGAAGAAGGCTCTCAACCAAGTAAATCACTCTCAGCAAAACC 158
    |||||
QY 121 ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC 180
    |||||
Db 159 ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC 218
    |||||
QY 181 AGCTCTGAAGAGCCACACCAACATACAAAGCAAACTCTCCAAGAAAAATTCCTCTCGA 240
    |||||
Db 219 AGCTCTGAAGAGCCACACCAACATACAAAGCAAACTCTCCAAGAAAAATTCCTCTCGA 278
    |||||
QY 241 GATCTGACCAAAACCTTGACCTCAAAATGAGAGAACCAACTGGGACAGTGCAGAG 300
    |||||
Db 279 GATCTGACCAAAACCTTGACCTCAAAATGAGAGAACCAACTGGGACAGTGCAGAG 338
    |||||
QY 301 CAGAAGGAAATGGA-----CCCGGGAAAAGGTCCAAACAG 338
    |||||
Db 339 GAGCAGGAAGGAATGGGACCCCGGGAAAGGAAGTNCACACAG 383
    |||||

```

RESULT 15

```

LOCUS AW465556
DEFINITION BP230019A20H7 Soares normalized bovine placenta Bos taurus cDNA
clone BP230019A20H7 5', mRNA sequence.
ACCESSION AW465556
VERSION AW465556.1 GI:7035661
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 545)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
Larson,J.H.
Bovine ESTs
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTACCTCTCAATAAG
Insert Length: 545 Std Error: 0.00
Plate: BP230019A20 row: H column: 7
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 545.
Location/Qualifiers
1..545
/organism="Bos taurus"

```

TITLE

JOURNAL

COMMENT

FEATURES

source

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:22:44 ; Search time 164.746 Seconds
(without alignments)
8185.526 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 atgttataatcgtgacaaa.....aagaaaggctaaagcaataa 2430

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	93.8	3.9	7218	1	US-08-232-463-14
C 2	85.6	3.5	2223	1	US-08-257-073-4
C 3	78.8	3.2	929	4	US-09-671-317-14
C 4	72.8	3.0	1001	4	US-09-671-317-439
C 5	66.6	2.7	396	4	US-09-640-173-53
C 6	66.6	2.7	396	4	US-09-713-550-53
C 7	66.2	2.7	2394	4	US-09-800-729-33
8	65.6	2.7	1696	4	US-09-835-811-1
9	65.6	2.7	2447	2	US-09-014-969-14
10	64.8	2.7	43795	3	US-08-742-185-101
11	64.2	2.6	240	1	US-08-628-417-6
12	64	2.6	1447	4	US-08-443-041A-27
13	63	2.6	674	4	US-09-620-405B-465
14	63	2.6	674	4	US-09-433-826B-465
15	63	2.6	674	4	US-09-604-287A-465
16	63	2.6	674	4	US-09-834-759-465
17	62.8	2.6	1051	3	US-09-245-041-10
C 18	62.6	2.6	118067	4	US-09-497-855A-32
C 19	62.2	2.6	16442	3	US-08-781-891-208
C 20	62.2	2.6	16442	4	US-09-619-166-208
21	61.6	2.5	249	4	US-09-621-976-1322
22	61.6	2.5	2608	4	US-09-904-615-16
23	61.6	2.5	3211	2	US-08-574-959A-8
24	61.6	2.5	3211	3	US-09-357-014-8
25	61.6	2.5	3901	2	US-08-574-959A-6
26	61.6	2.5	3901	3	US-09-357-014-6
27	61.4	2.5	282	3	US-09-461-697-205

28 61.4 2.5 306 3 US-09-461-697-203 Sequence 203, App
29 61.4 2.5 696 3 US-09-461-697-193 Sequence 193, App
30 61.4 2.5 699 3 US-09-461-697-191 Sequence 191, App
31 61.4 2.5 717 3 US-09-461-697-189 Sequence 189, App
32 61.4 2.5 774 3 US-09-461-697-187 Sequence 187, App
33 61.4 2.5 819 3 US-09-461-697-185 Sequence 185, App
34 61.4 2.5 1669 3 US-09-461-697-184 Sequence 184, App
35 60.8 2.5 1798 4 US-09-797-906-1 Sequence 1, Appli
36 60.8 2.5 12980 3 US-08-811-566-5 Sequence 5, Appli
37 60.8 2.5 12980 4 US-09-034-756-5 Sequence 1, Appli
38 60.4 2.5 5394 3 US-08-688-376-1 Sequence 1324, Ap
39 59.6 2.5 240 4 US-09-621-976-1324 Sequence 47, Appli
40 59.2 2.4 55298 4 US-10-204-708-47 Sequence 1, Appli
41 59.2 2.4 55298 4 US-09-491-356C-1 Sequence 207, App
42 59 2.4 231 3 US-09-461-697-207 Sequence 44, Appl
43 58.6 2.4 569 4 US-09-461-325-44 Sequence 44, Appl
44 58.6 2.4 569 4 US-10-012-542-44 Sequence 44, Appl
45 58.4 2.4 1276 3 US-09-177-325-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)833-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgt-F15
; US-08-232-463-14

Query Match 3.9%; Score 93.8; DB 1; Length 7218;

[illegible]

RESULT 2
US-08-257-073-4
; Sequence 4, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.

```

; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2570
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-06-257-073-4

Query Match          3.5%; Score 85.6; DB 1; Length 2223;
Best local similarity 68.6%; Pred. No. 6.1e-12;
Matches 118; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY      2088 AGAGCAAGCAGCTCAGAGAAAGAAAAATTCGAAGCAGCAGAGGAGGAGGAAAGGAAAGAAA 2147
Db      2016 AATATAGGAGAGAGAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAA 2075
QY      2148 TGAAGATAAACAAAAAGAAAAATGAAGATAAACAAAAAGAAAAATGAAGATAAACAGGAAAGAA 2207
Db      2076 AGAAGAAAAAGAAAAAGAAAAAGAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAGA 2135
QY      2208 AATGAAGATAAGATAAAGGAGAGAGAGCCAGCAAGAGAGAGCCACTGGACAGA 2259
Db      2136 AGAAGAAAAAGAAAAAGAAAAAGAAAGAAACAAGAGAAAGAAAGAAAGAAATA 2187

RESULT 3
US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62-US3-CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.mis1, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 634..652

```


OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-454-363 potential probe
NAME/KEY: misc_feature
LOCATION: 674..679,881..882,892..893
OTHER INFORMATION: n=a, g, c or t

US-09-671-317-14

Query Match 3.2%; Score 78.8; DB 4; Length 929;
Best Local Similarity 63.7%; Pred. No. 2.1e-10;
Matches 116; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 2061 TCITGCAAGACTACTCAAAATTGAAGCGAGAGCAAGCTCAGAGAAAGAAATTTCTGA 2120
Db 919 TCAGCGCATTTGCACTCAGCTGAGCUNVAGCGAGGANNCCATCTCAAGAGAGAGAGA 860
QY 2121 AGGAGGAG 2180
Db 859 AGAAG 800
QY 2181 AAG 2240
Db 799 AGAAG 740
QY 2241 AG 2242
Db 739 AG 738

RESULT 4
US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLERIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-242 : deletion AT
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-242.mis1, potential
; NAME/KEY: primer_bind
; LOCATION: 260..279
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 755..773
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_feature
; LOCATION: 795..800
; OTHER INFORMATION: n=a, g, c or t

US-09-671-317-439

Query Match 3.0%; Score 72.8; DB 4; Length 1001;
Best Local Similarity 70.0%; Pred. No. 7.4e-09;
Matches 98; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 2093 AAGCAGCTCAG 2152
Db 993 AAG 934
QY 2153 ATAAACAAAG 2212
Db 933 AAG 874
QY 2213 AAGATATAAGATAAAGGAAGA 2232
Db 873 AAG 854

RESULT 5
US-09-640-173-53/c
; Sequence 53, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G

Query Match 2.7%; Score 66.6; DB 4; Length 396;
Best Local Similarity 54.9%; Pred. No. 1.8e-07;
Matches 123; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 2023 CTGTTTAAACTCTCTCTAGGAGGACAGGAAAGCAAGTCTTTCAGAGACTACTCAAAATG 2082
Db 263 CTTTNTTGAATTAATAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 204
QY 2083 AAGCGAGAGCAAGCAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2142
Db 203 AA 144
QY 2143 GAAATGAAGATAAACAAAAAG 2202
Db 143 AA 84
QY 2203 AAG 2246
Db 83 AA 40

RESULT 6
US-09-713-550-53/c
; Sequence 53, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C4
CURRENT APPLICATION NUMBER: US/09/713,550
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 205
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-713-550-53

Query Match 2.7%; Score 66.6; DB 4; Length 396;
Best Local Similarity 54.9%; Pred. No. 1.8e-07;
Matches 123; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 2023 CTGTTTAAACTCTCTAGGAGCAGAGAAAGCAAGTCTTGCAAGACTACTCAAAATG 2082
DB 263 CTTTITNTGAATTAAANAAGGNAANAANAANAANNTAAANAANAANAANAANA 204
QY 2083 AAGCAGAGCAGCAGCTCAGAGAGAAAGAAATTTCTGAGGAGGAGAGAGAGAGAAA 2142
DB 203 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 144
QY 2143 GAAATGAAGATAAACAANAAGAAATGAAGATAAACAANAAGAAATGAAGATAAAGGA 2202
DB 143 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 84
QY 2203 AAGAAATGAAGATAAAGATAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2246
DB 83 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 40

RESULT 7

US-09-800-729-33
Sequence 33, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 2394
TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-729-33

Query Match 2.7%; Score 66.2; DB 4; Length 2394;
Best Local Similarity 60.1%; Pred. No. 5.4e-07;
Matches 110; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 2064 TGCAGACTACTCAAAATGAAGAGCAGCAGCAGCTCAGAGAGAGAGAGAGAGAGAG 2123
DB 2188 TTCAGAAATCCATAAGAGAGAGCGGTAACTTATGATAGAGAGAGAGAGAGAGAG 2247
QY 2124 AGGAG 2183
DB 2248 AAAAAAGGAG 2307
QY 2184 AGAAATGAAGATAAAG 2243
DB 2308 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 2367

QY 2244 GAA 2246
DB 2368 AAA 2370

RESULT 8

US-09-835-811-1
Sequence 1, Application US/09835811
Patent No. 6482936
GENERAL INFORMATION:
APPLICANT: HU, Song et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL0012228
CURRENT APPLICATION NUMBER: US/09/835,811
CURRENT FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1696
TYPE: DNA
ORGANISM: Human
US-09-835-811-1

Query Match 2.7%; Score 65.6; DB 4; Length 1696;
Best Local Similarity 56.5%; Pred. No. 6.4e-07;
Matches 122; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 2031 AACTCTCTAGGAGCAG 2090
DB 1472 ACCTGTCCCTCCCTCCCAAGATTAAAGGATCACTGTATAGATTAAAAA 1531
QY 2091 GCAAGCAGCTCAG 2150
DB 1532 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1591
QY 2151 AGATAAACAANAAG 2210
DB 1592 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1651
QY 2211 TGAAGATAAG 2246
DB 1652 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1687

RESULT 9

US-09-014-969-14
Sequence 14, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSES: Genetics Institute, Inc.
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

[illegible]

QY	2228	GAA	2230
Db	672	AAA	674

RESULT 15

```

US-09-604-287A-465
; Sequence 465, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS OF BREAST AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604, 287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 465
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-465

```

	Query Match	2.6%;	Score 63;	DB 4;	Length 674;
	Best Local Similarity	59.0%;	Pred. No. 1.9e-06;		
	Matches 108;	Conservative 0;	Mismatches 75;	Indels 0;	Gaps 0;
Qy	2048	CAGGAAAGCAAGTCTTTGC	AAGACTACTCAAATTTGA	AGCGAGACGACGCTCAGA	AAGA 2107
Db	492	CAGCAAAAGGNAGNACCT	TAGGAGATCCCATGGGAG	AAAAAAGATGACTCAGTT	TAAGGCCAA 551
Qy	2108	AGGAAAATTCTTGAAAGG	AGGAGCAGGAAGAAAGAA	ATAATGAAGATATAACA	AAAAAGAAA 2167
Db	552	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAA 611
Qy	2168	ATGAAGATATAACCAAAA	AGAAAATCAAGATAAAG	CAAAAAGAAAATGAAGA	TATAAGATAAG 2227
Db	612	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAA 671
Qy	2228	GAA 2230			
Db	672	AAA 674			

Search completed: June 22, 2004, 04:09:27
Job time : 167.746 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 00:29:50 ; Search time 994.629 Seconds
(without alignments)
11192.162 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 agttrtaactgctgacaaa.....aagaaaggctgaagcaataa 2430

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577.4	23.8	2607	16	US-10-189-507-3
2	577.4	23.8	4382	16	US-10-159-563-147
3	306	12.6	680	13	US-10-027-632-204539
4	306	12.6	680	13	US-10-027-632-204539
5	176.4	7.3	2500	13	US-10-342-887-427
6	176.4	7.3	2500	13	US-10-172-118-427
7	133.2	5.5	3027	15	US-10-295-573-1
8	132.8	5.5	2085	15	US-10-345-680-27
9	132.8	5.5	3494	15	US-10-345-680-25
10	131.6	5.4	1995	15	US-10-087-217-1
11	131.6	5.4	1995	15	US-10-087-217-5
12	131.6	5.4	3027	15	US-10-295-573-2
13	131.6	5.4	3027	15	US-10-295-573-4
14	129	5.3	526	9	US-09-864-761-12975

15	128.4	5.3	1995	15	US-10-087-217-3	Sequence 3, Appli
16	128.4	5.3	1995	15	US-10-087-217-7	Sequence 7, Appli
17	128	5.3	2877	15	US-10-295-573-3	Sequence 3, Appli
18	127	5.2	127	9	US-09-864-761-29538	Sequence 29538, A
19	111.2	4.6	1995	9	US-09-735-927-1	Sequence 1, Appli
20	111.2	4.6	1995	14	US-10-034-843-1	Sequence 1, Appli
21	111.2	4.6	1995	15	US-10-168-651-34	Sequence 34, Appli
22	111.2	4.6	1995	16	US-10-189-507-1	Sequence 1, Appli
23	111.2	4.6	2111	15	US-10-114-153-17	Sequence 17, Appli
24	111.2	4.6	2190	15	US-10-029-677-23	Sequence 23, Appli
25	111.2	4.6	12017	9	US-09-735-927-3	Sequence 3, Appli
26	109.6	4.5	1995	16	US-10-189-507-4	Sequence 4, Appli
27	109.6	4.5	2186	15	US-10-029-677-1	Sequence 1, Appli
28	84	3.5	31124	13	US-10-087-192-463	Sequence 463, App
29	81	3.3	625	13	US-10-027-632-179350	Sequence 179350,
30	81	3.3	625	15	US-10-027-632-179350	Sequence 45, Appl
31	80	3.3	2232	16	US-10-087-464-45	Sequence 45, Appl
32	79.6	3.3	305	9	US-09-864-761-19262	Sequence 19262, A
33	79.6	3.3	496	9	US-09-864-761-2534	Sequence 2534, Ap
34	79.2	3.3	37265	13	US-10-087-192-49	Sequence 49, Appl
35	79.2	3.3	39443	16	US-10-085-117-3113	Sequence 313, App
36	79	3.3	276	9	US-09-864-761-20595	Sequence 20595, A
37	79	3.3	462	9	US-09-864-761-3829	Sequence 3829, Ap
38	79	3.3	1728	9	US-09-527-267-3	Sequence 3, Appli
39	79	3.3	1728	16	US-10-189-507-2	Sequence 2, Appli
40	79	3.3	2308	9	US-09-927-267-2	Sequence 351, App
41	79	3.3	2366	13	US-10-302-172-351	Sequence 29, Appl
42	79	3.3	2551	10	US-09-842-758-29	Sequence 29, Appl
43	79	3.3	2551	13	US-10-174-333-29	Sequence 14, Appl
44	78.8	3.2	929	13	US-10-294-334-14	Sequence 15, Appl
45	78.6	3.2	143899	10	US-09-972-546-15	

ALIGNMENTS

RESULT 1

- US-10-189-507-3
- Sequence 3, Application US/10189507
- Publication No. US20030228633A1
- GENERAL INFORMATION:
- APPLICANT: ZOLLER, MARK
- APPLICANT: XU, HONG
- APPLICANT: STASZEWSKI, LENA
- APPLICANT: MOYER, BRYAN
- APPLICANT: PRONIN, ALEX
- APPLICANT: ADLER, JON ELLIOT
- APPLICANT: SALLANT, GUY
- APPLICANT: CALLAMARAS, NICHOLAS
- TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
- TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
- TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
- TITLE OF INVENTION: SMELL MODULATORS
- FILE REFERENCE: 078003-0291567
- CURRENT APPLICATION NUMBER: US/10/189,507
- CURRENT FILING DATE: 2003-02-12
- PRIOR APPLICATION NUMBER: 60/303,140
- PRIOR FILING DATE: 2001-07-06
- PRIOR APPLICATION NUMBER: 60/337,154
- PRIOR FILING DATE: 2001-12-10
- NUMBER OF SEQ ID NOS: 12
- SOFTWARE: PatentIn Ver. 2.1
- SEQ ID NO 3
- LENGTH: 2607
- TYPE: DNA
- ORGANISM: Homo sapiens
- US-10-189-507-3

Query Match 23.8%; Score 577.4; DB 16; Length 2607;
Best Local Similarity 64.3%; Pred. No. 8.4e-119;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
QY 617 TTCCAACAGCATAGATTACACAGATCGACTCTATCTCTCTGGCTCTTGTGTCGA 676

Db 782 TTCCCGAGCATGACCGCTGACCACTGATGATGCTATGCTGCTGCTG 841
Qy 677 CTCCTGCTTAACTGGAACCTGCTGTTTATACCACTGCGCTGCTTCCCATATCAA 736
Db 842 TGATGCGCTGGAATGGAACCTGCTGCTGATTCGCGTGGCGCTTCCCTTACCAGA 901
Qy 737 CGGAGACAAATACACTACTGCTGCTTATGCGGACATCATATGATGATCATCTACCTTT 796
Db 902 CCCGGAACAATCCACACCTGCTGCTGATGATGATGATGATGATGATGATGATGATG 961
Qy 797 ATGATATGCTATTTATCCAGCCGACCTGCTGCTGATGATGATGATGATGATGATGATG 856
Db 962 TGGACATACCGCTGCTCCAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021
Qy 857 ATTCGAATGAGTAAAGAAACACTACAGGACTTCTACAAATTTCACTGATGATGCTGCT 916
Db 1022 ACAAAGGACATGGAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1081
Qy 917 CAATAATACCAATTTGCTACCTCTTTTGGGTTTAAATCCCAATGTTAGAGCAA 976
Db 1082 GCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1141
Qy 977 ATAGATGTTAAAGTACACTTCAATTTTGAATTTATCATCACTAGAGTCTATAATGG 1036
Db 1142 CCCGCTGTTAAAGTACATGCTGCTTCTGCGAGTTTAAACGCGCTGGAATCCATCTCA 1201
Qy 1037 ACAAGACATATATACAGAGTTTATCGAACTGATGCTGCTGCTGCTGCTGCTGCTGCT 1096
Db 1202 GCAAGCTACGCTACAGGCTGCTACAGGCTGCTACAGGCTGCTGCTGCTGCTGCTGCT 1261
Qy 1097 TTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1156
Db 1262 TGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
Qy 1157 TGTATGATGGGAGGAAACAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1216
Db 1322 TTTAGATGGGAGGAAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1381
Qy 1217 TTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1276
Db 1382 TCACCATCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1441
Qy 1277 ATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1336
Db 1442 ATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501
Qy 1337 GAGAGCTACAGCAATCAGAACTACTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1396
Db 1502 GGGCGCCACCGCGGACAGACCTTACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1561
Qy 1397 TGAACAATTCTCCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1456
Db 1562 TGAATTTCTACAGATCCCCAAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621
Qy 1457 CATGGAGCTCTCAAGAATGCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1516
Db 1622 CTTGCACTCGAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1681
Qy 1517 TCCAGTTAGCCCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1576
Db 1682 TCGGCTGGACCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
Qy 1577 AGGTTGTGATACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1636
Db 1742 AGGCTGTGACCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801
Qy 1637 TGCCTGTGATCTTGTCTGCAAAAGGAGAAATTTGCAAGGAAATGATATCATCAAGC 1696
Db 1802 TGCCCAAGGACTATGCTGCAAGGAGGAGATCGGCGCTGAGATGATCATCATCCAG 1861
Qy 1697 ATGAGAGTCCCAAGTTCTTGGAGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1756

Db 1862 CAGGCAAGTGCAGCTTCTGGCGCCCTGATGGAAATCTGCTGCTGCTGCTGCTGCTG 1921
Qy 1757 CTGGGTCGGTGTTCGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCGTGGAACTG 1816
Db 1922 CTGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
Qy 1817 CCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1876
Db 1982 CCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2041
Qy 1877 AAATCTAGTGCATTTATCAGATTTCTGAAAGATCTCATGAGAAACCCAGAGTCTTT 1936
Db 2042 AGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2101
Qy 1937 TAAAGCAGAGGCTAAGACCGCAGAG 1963
Db 2102 TGGAAGACNACATTAAGCCCAAGAGG 2128

RESULT 2

US-10-159-563-147
; Sequence 147, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 4382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-147

Query Match 23.8%; Score 577.4; DB 16; Length 4382;
Best Local Similarity 64.3%; Pred. No. 1.1e-119;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

Qy 617 TTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTGCTGGCTTTGCTTTGCTCA 676
Db 1983 TTCCCCAGAGCATTCACCCGCTGACCACTGATGATGCTCTATGGCTGCTTCTGCTGG 2042
Qy 677 CTCCTTGCCTTAACCTGGAACCTGCTGCTTATACCACTCGGCTGCTTCCCATATCAA 736
Db 2043 TGATGGCTTGGAAATGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2102
Qy 737 CGCGAGACAAATACATCACTACTGCTGCTTATGCGGACATCATATGATATCATCTTACCTTT 796
Db 2103 CCCCGAGACATCCACCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2162
Qy 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGAAGAGGAGGAGACATAATAGTGG 856
Db 2163 TGGACATCACCGTGTTCAGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2222
Qy 857 ATTCAAATGAGCTAAGAGAAACACTACAGGACTTCTACAAAATTTTCAGTTGATGCTCGCAT 916
Db 2223 ACAAAGAGACATGCAATTAACCTACCTGAACTCTCGCGCTTCAAGATGACCTGCTCA 2282
Qy 917 CAATTAATACCAATTTGATATTTGCTTACCTCTCTCTTTGGGTTTAAATCCAAATGTTAGACAA 976
Db 2283 GCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2342
Qy 977 ATGAGATGTTAAAGTACACTTCATTTTGAATTTAAATCATCATCAGCTAGAGTCTATAATGG 1036

PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 2085
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2085)
US-10-345-680-27

Query Match 5.5%; Score 132.8; DB 15; Length 2085;
Best Local Similarity 49.2%; Pred. No. 3.3e-19;
Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;

QY 856 GATTCAATGAGCTAAGGAAACACTACAGGACTTCTCAAAATTTTCAGTTGATGTCGA 915
Db 703 GATACCAACAGCTGTGGCAGCATTAACAAGACGACACAGCTTCAAGCTGGATGTG 762
QY 916 TCAATAATACCAATTTGATATTTGCTACCTCTCTTTGGGTTTA---ATCCAATGTTTGA 972
Db 763 TCCCTGGTCCCAACGACCTGGCTTACTTAAAGTGGGCACAACTACCCAGAGTGGG 822
QY 973 GCAATATAGAGTGTAAAGTACACTTCATTTTTTGAATTTAATCATCACTACAGACTATA 1032
Db 823 TTCAACCGGCTACTGAAGTTTCCCGGCTCTTTGAATTTTTCACCGCACAGACAAGG 882
QY 1033 ATGGCAAAAGCATATCTACAGAGTTATCGAACAACTGGATCTGCTGTTTATTCTG 1092
Db 883 ACCAACTACCCCAATATGTCAGGATGGGAATCTGGTCTGTGACATTTCTCATCATC 942
QY 1093 CACATTAATGCCCTGTGTTTATTACTGGGCTTCAAATATGAAGGATTTGGCACTACTAGA 1152
Db 943 CACTGGATGCCCTGCATCTACITTTGCCATTTCCAAATTCATTGGTTTGGGACAGACTCC 1002
QY 1153 TGGGTGT-----ATGATGGGGAAGGAACAGATCTGAGA 1188
Db 1003 TGGGTCTACCCAAACATCTCAATCCAGAGCATGGCGGCTCTCCAGGAAGTACATTTAC 1062
QY 1189 TGTATTATTGGGCAGTTCGAATCTTAATACCATTTGGTGGCTTCCAGAACCAAACT 1248
Db 1063 AGTCTACTGGTCCACCTTGACCTTACCACTTTGGTGGACACCCACCCCGGTGAA 1122
QY 1249 TTATTTGAAATGTTTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGT 1308
Db 1123 GATGAGGAGTATCTCTTTGGTGTGAGACTTCTTGGTGGGTGTTCTGATTTTGGCCACC 1182
QY 1309 TTAATTTGGTCAGATGAGATGTGATTTGGAGCAGCTACAGCAATCAGAACTACTTCCGC 1368
Db 1183 ATTGTGGGCAATGTGGCTCCATGATCTCGAATATGAATGCTTCACGGGACAGTTCCAG 1242
QY 1369 GCCTGATGATGACACCACTTGCCTACATGAACAATTTACTTCCATTTCTAAACTTGTGCAA 1428
Db 1243 GCCAAGATTGATTCATCAAGCAGTACATGCACTTCGCGAAGTCCCAAGGACTTGGAG 1302
QY 1429 AGCGAGTTCGGACTTGGTATGAATATACATGGGACTCTCAAGATGCTAGATGAGTCT 1488
Db 1303 ACGGGGTTATCCGGTGGTTTGAATCTACCTGTGGGCCAACAAAGAGACGGTGGATGAGAG 1362
QY 1489 GATTTCGTTAAGACCCCTACCAACTACGGTCCAGTTAGCCCTCCGCAATTTGATGTGAATCT 1548
Db 1363 GAGGTCTCAAGAGCTTCCAGACAGAGCTGAAGCTGAGATCGCAATCAACGTGCACCTG 1422
QY 1549 AGCATCATCAGAAAGTCGACTTGTTCAGGGTTGTGATACACAGATGATTTATGACATG 1608
Db 1423 GACACGCTGAAGAAGGTTCCGATCTTCCAGGACTGTGAGGACGGGCTGCTGGTGGAGCTG 1482
QY 1609 TTGCTAAGATTGAATCCGTTCTCTATTTCCTGGTGACTTTTCTGTCAAAAGGAGAA 1668

Db 1483 GTGCTGAAGCTGGACCCACTGTGTTGAGCCCTGGGATTAATATCTGCAAGAGGAGAT 1542
QY 1669 ATTGGCAAGGAAATGTATATCATCAAGCATGGAAGTCCAAGTTCTTTGAGGCCCTGAT 1728
Db 1543 ATTGGGAAGGAGATGTATCATCAACAGGGAAGCTGGCCGTGGTGGCTGATGATGGG 1602
QY 1729 GGTACTAAAGTTCTGGTTACTCTGAAGCTGGGTGGTGGTGGTGGAGAAATCAGCCTTCT- 1787
Db 1603 GTCACCCAGTTCGTGGT---CCTCAGCATGGCAGCTACTTCGGGGAGATCAGCATCTG 1659
QY 1788 AGCAGCAGGAGGAGAAACCGTCCAACTGC 1817
Db 1660 AACATCAAGGGAGCAAGTCGGGAAACCGC 1689

RESULT 9

US-10-345-680-25
; Sequence 25, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MF102-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3486
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(2124)
US-10-345-680-25

Query Match 5.5%; Score 132.8; DB 15; Length 3486;

Best Local Similarity 49.2%; Pred. No. 4.4e-19;

Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;

QY 856 GATTCAATGAGCTAAGGAAACACTACAGGACTTCTCAAAATTTTCAGTTGATGTCGA 915
Db 742 GATACCAACAGCTGTGGCAGCATTAACAAGACGACACAGCTTCAAGCTGGATGTGTTG 801
QY 916 TCAATAATACCAATTTGATATTTGCTACCTCTCTTTGGGTTTA---ATCCAATGTTTGA 972
Db 802 TCCCTGGTCCCAACGACCTGGCTTACTTAAAGTGGGCACAACTACCCAGAGTGGG 861
QY 973 GCAATATAGATGTTAAAGTACACATTTTGAATTTTGAATTAATCATCACTAGAGTCTATA 1032

1465 TCTCAAGAATGCTAGATGAGTCTGATTTGGCTTAAGACCCCTACCACTACGGTCCAGTTA 1524
 1261 AATAAGAGACAGTAGATGACAGAGAGTCTCCAGAACCTGCCAGAAAGCTCAGGGCT 1320
 1525 GCCCTCGCCATGATGTGAACCTTACGATCATCAGCAAAAGTGAATTGTTCAAGGGTTGT 1584
 1321 GAGATAGCCATTAAATGTTCACTTTGCTCCACTCTGAAGAAAGTGGCATAATCCAGGATTGT 1380
 1585 GATACACAGATGATTTATGACATGTTTGTGTAAGATTGAAATCCGTTCTCTATTGCTCGGT 1644
 1381 GAAGCTGGCTACTGTGGAGTGGTACTGAAGCTTCGTCCTCAGGTCTTTAGTCTTGA 1440
 1645 GACTTTGTTGCAAAAAGGAGGAAATGGCAAGAAATGTATATCATCATCAAGCATGAGAA 1704
 1441 GATTATATTGCGGTAAAGGGGACATTTGGCAAGAAATGTATCATCATCAAGGAGGCAAG 1500
 1705 GTCCAGTTCTTTGAGGCCCTGATGTGTAAGATTGAAATGCTGTGTTCTCTGTTGCTGG 1760
 1501 TTGGCTGGTGTAGCTGATGATGATGGCTGACTCAGTATGCCCTTGTCTCAGCTGGAGCTGC 1560
 1761 GTGGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGA--GGAAACCGTGAAGTGC 1818
 1561 TTTGGTGAGATTAGTATCCCTTAACATTTAAGGTAGCAAAATGGCAATCGAAGTACTGCT 1620
 1819 AATGTGTGCCCCACGGTTTGGCAATCTTTAACTCTAGACAAAGACCCCTCCAAGAA 1878
 1621 AATATCCGTAGCTGGGCTACTCAGATCTCTCTGCTTGTCCAAAGACGATCTTATGGAA 1680
 1879 ATTCTAGTCAATTATCAGATCTCTGAAGGATCTCATGAAGAAAGCCAGAGTGCCTTTA 1938
 1681 GCTGTAACTAGTATCTGTATGCCAGAGGCTCTGGAGGACGGGTAGGAGATCCTG 1740
 1939 AAGCAGAGGCT 1950
 1741 ATGAAGGAAGGT 1752

RESULT 11
 US-10-087-217-5
 ; Sequence 5, Application US/10087217
 ; Publication No. US20030100059A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aptus Genomics, Inc.
 ; APPLICANT: YAO, Yong
 ; APPLICANT: CAO, Liang
 ; TITLE OF INVENTION: No. US20030100059A1 Cell-Based Assays for G-Protein-Coupled Receptors
 ; FILE OF INVENTION: Activities
 ; FILE REFERENCE: 53735-5004-US
 ; CURRENT APPLICATION NUMBER: US/10/087,217
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: 60/330,663
 ; PRIOR FILING DATE: 2001-10-26
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 1995
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1992)
 ; OTHER INFORMATION:
 US-10-087-217-5

Query March 5.4%; Score 131.6; DB 15; Length 1995;
 Best Local Similarity 46.7%; Pred. No. 6.1e-19;
 Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;
 652 TATCTCTGTGGCTTCTGCTTGTGCTCACTCTTGTGCTTAACTGAAGTCTGCTTTATACCA 711
 424 TATTACCGTTGGTTGTTGTCATTGCCATGCTCTCTTACAACTGGTGGCTTTGGTG 483

QY 712 CTGCGCTGTGTTCCCATATCAAAACCGCAGACAACATACACTACTGCTTATTCGGAC 771
 DB 484 GCCAGAGCCTGTTTCACTGATCTACAGAGAACTATTTTGTGGTATGGCTGGCTGGAC 543
 QY 772 ATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTT 831
 DB 544 TACTTCTCAGACATGTTCTATATCGCAGACTCATCATTCGGCTGCGCAGAGC---TTC 600
 QY 832 GTAAGAGGAGAGACATAATAGTGGATTCAAAATGAGCTTAAGGAAACACTACAGGACTTCT 891
 DB 601 CTAGAACAGAGGGCTCTTGGTCAAGAGATCCCAAGAAATTCGAGACAACTATATTCACACT 660
 QY 892 ACAAAATTTCACTGTTGGATGTCGCATCAATATACATTTGATATTTGCTACTCTCTCTTT 951
 DB 661 TTGCAGTTCAAAATTTGGATGTTGGCTTTCTATCATTCACCTGACCTTATTTTGTCTGTG 720
 QY 952 GGGTT---TAATCCAAATGTTTAGAGCAAAATAGAGTGTAAAGTACACTTCATTTTGTAA 1008
 DB 721 GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTGCCCGTATGTTTGG 780
 QY 1009 TTTAATCATCACTAGAGTCTATTAATGGACAAGCATATATCTACAGATTTATTTCGAACA 1068
 DB 781 TTCTTTGACCCGACTGAGACAGCACGCCAGCTACCCCAACATCTTCCGAATCAGCAATCTG 840
 QY 1069 ACTGATATCTTGTGTTTATTTCTGCACATTAATGCTGTGTTTATTTACTGGGCTTCAAA 1128
 DB 841 GTCCTTTACATCTTGGTCATCATCCACTGGAATGCTTGTA TTTATTATGTTATTCTTAAG 900
 QY 1129 TATGAAGAAATGG-----CACTACTAGATGGGTGATGAT 1164
 DB 901 TCCATTGGCTTTGGAGTTGACACCTGGGTTTACCCCAACATTACTGACCCCTGAATATGGC 960
 QY 1165 GGGGAAGGAAACGAGTATCTGAGATGTTTATTTATTTGGGAGTTTCAAACTTTTAATACCATT 1224
 DB 961 TACCTGGCTAGAGAGTACATTTACTGTTCTTTACTGTTCCACACTGACCCCTCACCACATT 1020
 QY 1225 GGTGGCTTCCAGAACCAAACTTTATTTGAAATGTTTTCAACTCTTGAATTTTTTT 1284
 DB 1021 GGAGAGACACACCCCTGTAAAGGATGAGGAGTACCTATTGTCATCTTTGACTTCTTG 1080
 QY 1285 TCTGAGTTTTTGTGTTCTCCAGTTTAAATTTGGTCAAGATGAGATGATGATTTGGAGCAGCT 1344
 DB 1081 ATTGTTGCTCTCATCTTTGGCCACTATTGTTGGAATGTTGGGCTCCATGATCTCCAACTG 1140
 QY 1345 ACAGCCAATCAGAACTACTTCCGCGCTGCATGATGACACCAATTCCTACATGAACAAAT 1404
 DB 1141 AATGCCACAGCAGCAGAGTTCCAGSCCAAGATTGATGCTGTCAAAACACTACATGCAAGTTC 1200
 QY 1405 TACTCCATTCTTAACTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATATACATGAGGAC 1464
 DB 1201 CGAAAGGTGAGCAAAAGACATGGAAGCCAAAGGTCATCAAAATGTTGATCTTTGTTGGACC 1260
 QY 1465 TCTCAAGAAATGCTAGATGAGTCTGATTTGTTTAAAGACCTTACCACACTACGCTCCAGTTA 1524
 DB 1261 AATAGNAGACAGTATGAGCAGAGAGTCTTCAAGAACCTGCCAGCAAGCTCAGGGCT 1320
 QY 1525 GCGCTCGCAATGATGTGAACCTTTCAGATCATCAAGCAAGTGGCTTGTTCAGGGTTGT 1584
 DB 1321 GAGATAGCCATTAAATGTTTCACTTGTCCACTCTCTGAAAGAAAGTCCGATATTCAGGATTGG 1380
 QY 1585 GATACACAGATGATTTATGACATGTTTGTGTAAGATTGAAATCCGTTCTCTATTGCTGCTGT 1644
 DB 1381 GAAGCTGGCTTACTGGTGGAACTGGTACTGAAGCTTCGTCCTCAGGTCTTTAGTCTTGA 1440
 QY 1645 GACTTTGTCTGCAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGAGAA 1704
 DB 1441 GATTATATTGCGGTAAAGGGGACATTTGGCAAGGAAATGTATCATCATCAAGGAGGCAAG 1500
 QY 1705 GTCCAAAGTTCTTGGAGGCCCTGATGGTACTAAGTCTCTGGT---TACTCTCAAGCTGG 1760
 DB 1501 TTGGCAGTGGTATGATGATGCGGTGACTAGTATGCCCTGCTCTCAGCTGGAGCTGC 1560
 QY 1761 GTCGGTGTGTTGGAGAAATCAGGCTTCTTAGCAGCAGGAGGA--GGAAACCGTCCAACTGCC 1818

1561	TTTGGTGAGATTAGTATPCTTAACTTAAGGGTAGCAAAATGGCAATCGACGTACTGCT	1620
Db		
1819	AATGTGTGGTCCACCGGGTTGGCAATCTTTTAACTCTAGACAAAAAGACCCCTCCAGAA	1878
Qy		
1621	AATATCGTAGGCTGGGCTACTCAGATCTCTCTGTGTTGCCAAGGACGATCTTATGGAA	1680
Db		
1879	ATTCTAGTGCAATTATCCAGATTCTGAAGAATCCTCATGAAGAAACCCAGAGTCTTTTA	1938
Qy		
1681	GCGTAACTCAGTATCTCTGATGCCAAGAGGTCTTGGAGAACGGGGTAGGGAGATCCTG	1740
Db		
1939	AAGCAGAAAGGCT	1950
Qy		
1741	ATGAAGATGGGT	1752
Db		

```

RESULT 12
US-10-295-573-2
; Sequence 2, Application US/10295573
; Publication No. US20030157571A1
; GENERAL INFORMATION:
;
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schaack, Jerome
;
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS
;
; FILE REFERENCE: UTC-07536
;
; CURRENT APPLICATION NUMBER: US/10/295,573
;
; CURRENT FILING DATE: 2002-11-15
;
; PRIOR APPLICATION NUMBER: 60/332,494
;
; PRIOR FILING DATE: 2001-11-16
;
; NUMBER OF SEQ ID NOS: 8
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 2
;
; LENGTH: 3027
;
; TYPE: DNA
;
; ORGANISM: Rattus norvegicus
;
US-10-295-573-2

```

Db	1180	GTCCTTTACATCTTTGGTCATCATCCACTGGAATGCTTGTATTTATTATGTATTTCTTAAG	12339
Qy	1129	TATGAAGGAATTGG-----CACTACTAGATGGGTGTATGAT	1164
Db	1240	TCCATTGGCITTTGGAGTTGACACCTGGGTTTACCCCAACATTACTGACCTGAATGGC	1299
Qy	1165	GGGGAAGAAACGAGTATCTGAGATGTTATATTGGCAGTTCGAACTTTAAATTACCAATT	1224
Db	1300	TACCTGCTAGAGAGTACATTATCTGCTTTACTGTGTCCACACTGACCCCTCACCAACATT	1359
Qy	1225	GGTGGCCTTCCAGAACCCACAAACTTTTATTTGAATTTGTTTTTCAACTCTTTGAATTTTTT	1284
Db	1360	GGAGAGACACCACCCCCTGTAAAGATGAGAGTACCTATTGTCTCATCTTTGACTTCTTG	1419
Qy	1285	TCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGAGATGATGATTTGAGCAGCT	1344
Db	1420	ATTGGTGTCTCTATCTTTTGGCATTATTTGTGGGAAATGTGGGCTTCCATGATCTCCAACTG	1479
Qy	1345	ACAGCCAAATCAGAACTACTTTCGGCGCTGCATGGATGACACCACTTGCCTACATGAACAAT	1404
Db	1480	AATGCCACACGACGAGTTTCCAGGCCCAAGATTGATGCTGTCAACACTACATGCAAGTTC	1539
Qy	1405	TACTCCAATTCCTAAACTTGTGC AAAACGAGTTTGGACTTGTGATGAATATACATGGAC	1464
Db	1540	CGAAAGGTCAGCAAAAGACATGGAAGCCAGGTCATCAAAATGGTTTGACTACTTGTGGACC	1599
Qy	1465	TCITCAAAGATGCTAGATGAGTCTGATTTGCTTAAAGACCCTACCAACTACGGTCCAGTTA	1524
Db	1600	AATAAGAAACACGATGATGAAGCAGAGAGTCCCTCAAGAACTGCGCAGCAAGCTCAGGGCT	1659
Qy	1525	GCCTCGCCATTGATGTGAACTTTCAGCATCATCAGCAAAAGTCGACTTTGTTCAAGGGTTGT	1584
Db	1660	GAGATAGCCATTAAATGTTCACTTTGCCACTCTCAAGAAAGTGGGCATATTCCAGGATTGG	1719
Qy	1585	GATACACAGATGATTATGACATGTTGCTTAAGATTGAAATCCGTTCTCTATTGTCCTGGT	1644
Db	1720	GAAGCTGGCCTACTGTGGAACTGGTACTGAAGCTTCGTCCTCAGGTCCTTAGTCTCTGGA	1779
Qy	1645	GACTTTGCTGCAAAAAGGGAGAGAAATTTGGCAAGAAATGTATATCATCAAGATGAGAA	1704
Db	1780	GATTATATTTCGCGTAAGGGGACATTGGCAAGGAAATGTACATCATCAAGGAGGCAAG	1839
Qy	1705	GTCCAAGTCTTTGGAGGCCCTGATGTGACTAAAGTTCTGGT----TACTCTGAAGAGCTGG	1760
Db	1840	TTGGCACTGGTAGCTGATGATGGCGTGACTTCAGTATGCGCTTGCTCTCAGCTGGGAGCTGC	1899
Qy	1761	GTGGGTGTTTGGAGAAATCAGCCCTCTAGCAGCAGGAGGA--GGAAACCGTCCAACTGCC	1818
Db	1900	TTTTGGTCAGATTAGTATCCTTTAACTTAAGGGTAGCAAAATGGGCATCGACGTACTGCT	1959
Qy	1819	AATGTGGTGGCCACCGGTTTGGCAATCTTTTAACTCTAGACAAAGAACCTTCCAGAA	1878
Db	1960	AATATCCGTAGCCTGGGCTACTCAGATCTCTTCTGCTTGTCTCAAGGACGATCTTATGGAA	2019
Qy	1879	ATTCTAGTCATTATCCAGATTCTGAAGAGATCCTCATGAAGAAAGCCAGAGTGTCTTTTA	1938
Db	2020	GCTGTAACTCAGTATCTCTGATGCCAAGAGGTCCTGGAGAACGGGTAGGAGATCTCTG	2079
Qy	1939	AAGCAGAGGCT	1950
Db	2080	ATGAAGATGGGT	2091

RESULT 13
US-10-295-573-4
; Sequence 4, Application US/10295573
; Publication No. US20030157571A1
; GENERAL INFORMATION:
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schaack, Jerome
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS

FILE REFERENCE: UTC-07536
CURRENT APPLICATION NUMBER: US/10/295,573
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/332,494
PRIOR FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 3027
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-295-573-4

Query Match 5.4%; Score 131.6; DB 15; Length 3027;
Best Local Similarity 46.7%; Pred. No. 7.6e-19; Indels 36; Gaps 5;
Matches 622; Conservative 0; Mismatches 674

QY 652 TATCTCTGTGGCTCTTGCTTGTCATCTTGCCCTATTAACCTGGAACCTGCTGGTTTATPACA 711
Db TATTACCGTTGGTTGTTGTCATTGCCATGCCCTGTTCTTTAGCACTGGTGCCTGTTGGTG 822

QY 712 CTGCGGCTGCTCTCCATATCAACCGGAGACACATACACTACTGCGCTTATTCGGGAC 771
Db 823 GCCAGAGCCCTGCTTCAGTGTACAGAGAACTATTTGTGATGCTGGTGGTGGAC 882

QY 772 ATCATATGTCATATCATCTACCTTTATGATATGCTATTTATCCAGCCCAAGACTCCAGTTT 831
Db 883 TACTTCTCAGACACTGCTATATATCGCAGACCTCATCTTCGGCTGCGCACAGGC---TTC 939

QY 832 GTAAGAGGAGGACATAATAGTGGATTCAATAGCTAAGTAAGGAACACTACAGGACTTCT 891
Db 940 CTAGAACAGGGGCTCTTGTCCTCAAGATCCCAAGAAATTCGAGACAACTATATTACACT 999

QY 892 ACAAAATTTTCAGTTGGATGTCGATCAATAATACCAATTTGATATTTGCTACCTCTCTTT 951
Db 1000 TTGCGATTCAATTTGATGTTGGCTTTATGCTATTCCTATTCCTATTTGCTGTG 1059

QY 952 GGTTT---TAATCCAAATGTTTAGAGCAATPAGGATGTTAAAGTACACTTCATTTTTTGAA 1008
Db 1060 GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTGCCCGTATGTTGAG 1119

QY 1009 TTTAATCATCACCTAGTACTATAATGGAACAGCATATATCTACAGAGTTATTCGAACA 1068
Db 1120 TTCTTTGACCGCACTGAGACACGCCAGCTACCCCAACATCTTCGGAATCAGCAATCTG 1179

QY 1069 ACTGGAATCTGCTGTTTATCTGCAATTAATGCGCTGCTTTATTTACTGGGCTTCAAA 1128
Db 1180 GTCTTTTACATCTGCTCATCCATCCATCGAATGCTTGTTATTTATGTTATTTCTAAG 1239

QY 1129 TATGAAGGAATTGG-----CACTACTAGATGGGTGATGAT 1164
Db 1240 TCCATTGGCTTTGGAGTTGACACCTGGGTTTACCCCAACATTACTGACCTGAATATGGC 1299

QY 1165 GGGGAAGGAACAGTATCTGAGATGTTATTTATGGGCACTTCGAACCTTTAATTTACATT 1224
Db 1300 TACTGCTGAGAGTACATTTACTGCTTTTACTGCTCCACATGACCTCACCACCAATT 1359

QY 1225 GGTGCGCTTCAGAACCAAACTTTATTTGAAATTTGTTTTCACACTCTTTGAAATTTTTT 1284
Db 1360 GGAGAGACACACCCCTGTAAAGGATGAGGAGTACCTATTTGTCTATCTTTGACTTCTTG 1419

QY 1285 TCTGAGTTTTTGTCTTCCAGTTTAAATTTGTCAGATGAGATGATGTTGGAGCAGCT 1344
Db 1420 ATTGGTGTCTTCATCTTTGCGCACTATTGTGGAAATGTGGGCTCCATGATCTCAACATG 1479

QY 1345 ACAGCCATCAGAACTACTTCGCGCTGTCATGATGACACCACTATGCTACATGAACAAT 1404
Db 1480 AATGCCACAGCAGAGTTCCAGGCCAAGATTGATGCTGTCAACACTACATGCACTTC 1539

QY 1405 TACTCCATTCCTAACTTTGTCAAAAGGAGTTCCGACTTGGATGATGATATACATGGGAC 1464
Db 1540 CGAAAGGTTCAGAAAGACATGGAAGCCCAAGGTCAATCAATGGTTGACTACTTGTGGACC 1599

RESULT 14
US-09-864-761-12975
; Sequence 12975, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn. Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

QY 1465 TCTCAAGAATGCTAGATGAGTCTGATTGTTTAAAGACCCCTACCACTAAGGTCCAGTTA 1524
Db 1600 AATAAGAGACAGTAGATGACGAGAGAGTCTCTCAAGAACCTCCAGCAAGCTCAGGGCT 1659

QY 1525 GCCCTCGCCATTGATGTGAACCTTCAGCATCATCAGCAAGAGTCTGTTTCAAGGTTGT 1584
Db 1660 GAGATAGCCATTAAATGTTTCACTTCTGTCACCTCTGAAGAAAGTGGCATAATTCAGGATGT 1719

QY 1585 GATACACAGATGATTATTATGACATGTTCTAAGATTGAAATCCGTTCTCTATTTCCTGGT 1644
Db 1720 GAAGCTGCTACTGTTGGAACTGGTACTGAAGCTTCTGCTCTCAGGCTCTTTAGTCTTGG 1779

QY 1645 GACTTTGTCTCAAAAAGGGAGAAATTTGGCAAGAAATGTATATCATCAAGCATGGAGAA 1704
Db 1780 GATTATATTTCCTGTAAGGGGACATTTGGCAAGAAATGTATCATCATCAAGGAGGCAAG 1839

QY 1705 GTCAAGTTCTTGAGGCGCCCTGATGCTAGTAAAGTTCTGCT---TACTCTGAAGCTGG 1760
Db 1840 TTGCGAGTGGTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899

QY 1761 CTCGCTGTTTTCGAGAAATCAGCCTTTCTAGCAGCAGGAGGA--GGAAACCGTCCGAAGTCC 1818
Db 1900 TTTGTTGAGATTAGTATCTTTAACTTAAGGTTAGCAAAATGGCAATCGACGTACTGCT 1959

QY 1819 AATGTTGGTGGCCCGGGTTGCTTCCAAATCTTTTAACTCTAGCAAAAGACCCCTCCAAGAA 1878
Db 1960 AATATCCCTAGCTGGGCTACTCAGATCTCTCTGCTTGTCTCAAGGAGCATCTTATGAA 2019

QY 1879 ATTCTAGTGCATTATCCAGATTCTGAAAGGATCTCATGAAGAAAGCCAGAGTGTCTTTA 1938
Db 2020 GCTGTTACTGATGATCTGATGCTGCAAGAGGCTCTGAGGAGCGGGTATGAGATCCTG 2079

QY 1939 AAGCAGAAAGGCT 1950
Db 2080 ATGAAGGAAGGT 2091


```
Db 1441 GATTATATTGCCGTAGGGGGACATTGGCAGGAATGTACATCATCAGGAGGCAAG 1500
Qy 1705 GTCCAAAGTTCTTGGAGGCCCTGATGTACTAAAGTTCTGGT----TACTCTGAAGCTGG 1760
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCTTGTCTCAGCTGGGAGCTGC 1560
Qy 1761 GTCGGTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAAACCGTCGAACCTGCC 1818
Db 1561 TTTGGTGAGATTAGTATCCTTAACATTAGGGTAGCAAAATGGGCAATCGACGTACTGCT 1620
Qy 1819 AATGTGGTGGCCCAACGGGTTTGCCAAATCTTTTAACTCTAGACAAAAAGACCCCTCCAAGAA 1878
Db 1621 AATATCCGTAGCCTGGGCTACTCAGATCTCTTCTGCTTGTCCAAGGACGATCTTATGGAA 1680
Qy 1879 ATTCTAGTGCATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTA 1938
Db 1681 GCTGTAACTGAGGCTCCTGATGCCAAGAGGCTCTGGAGAACGGGGTAGGAGATCCTG 1740
Qy 1939 AAGCAGAAGGCT 1950
Db 1741 ATGAAGGAAGGT 1752
```

Search completed: June 22, 2004, 09:37:22
Job time : 1005.63 secs

This Page Blank (uspto)